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(21) International Application Number: PCT/US98/10313 (22) International Filing Date: 20 May 1998 (20.05.98) (30) Priority Data: 60/047,194 20 May 1997 (20.05.97) US (71) Applicant: CORNELL RESEARCH FOUNDATION, INC. [US/US]; Suite 105, 20 Thornwood Drive, Ithaca, NY 14850 (US). (72) Inventors: ZHU, Hai-Ying; 681 Castle Street, Geneva, NY 14456 (US). LING, Kai-Shu; 170 William Street, Geneva, NY 14456 (US). GONSALVES, Dennis; 595 Castle Street, Geneva, NY 14456 (US). (74) Agents: GOLDMAN, Michael, L. et al.; Nixon, Hargrave, Devans & Doyle LLP, Clinton Square, P.O. Box 1051, Rochester, NY 14603 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: GRAPEVINE LEAFROLL VIRUS (TYPE 2) PROTEINS AND THEIR USES (57) Abstract <p>The present invention relates to isolated proteins or polypeptides of grapevine leafroll virus (type 2). The encoding DNA molecules either alone in isolated form or in an expression system, a host cell, or a transgenic grape plant are also disclosed. Other aspects of the present invention relates to a method of imparting grapevine leafroll resistance to grape and tobacco plants by transforming them with the DNA molecules of the present invention, a method of imparting beet yellows virus resistance to a beet plant, a method of imparting tristeza virus resistance to a citrus plant, and a method of detecting the presence of a grapevine leafroll virus, such as GRLaV-2, in a sample.</p>		

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GRAPEVINE LEAFROLL VIRUS (TYPE 2) PROTEINS AND THEIR USES

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FIELD OF THE INVENTION

The present invention relates to grapevine leafroll virus (type 2) proteins, DNA molecules encoding these proteins, and their uses.

BACKGROUND OF THE INVENTION

The world's most widely grown fruit crop, the grape (*Vitis sp.*), is cultivated on all continents except Antarctica. However, major grape production centers are in European countries (including Italy, Spain, and France), which constitute about 70% of the world grape production (Mullins et al., Biology of the Grapevine, Cambridge, U.K.:University Press (1992)). The United States, with 300,000 hectares of grapevines, is the eighth largest grape grower in the world. Although grapes have many uses, a major portion of grape production (~80%) is used for wine production. Unlike cereal crops, most of the world's vineyards are planted with traditional grapevine cultivars, which have been perpetuated for centuries by vegetative propagation. Several important grapevine virus and virus-like diseases, such as grapevine leafroll, corky bark, and *Rupestris* stem pitting, are transmitted and spread through the use of infected vegetatively propagated materials. Thus, propagation of certified, virus-free materials is one of the most important disease control measures. Traditional breeding for disease resistance is difficult due to the highly heterozygous nature and outcrossing behavior of grapevines, and due to polygenic patterns of inheritance. Moreover, introduction of a new cultivar may be prohibited by custom or law. Recent biotechnology developments have made possible the introduction of special traits, such as disease resistance, into an established cultivar without altering its horticultural characteristics.

Many plant pathogens, such as fungi, bacteria, phytoplasmas, viruses, and nematodes can infect grapes, and the resultant diseases can cause substantial losses in production (Pearson et al., Compendium of Grape Diseases, American Phytopathological

Society Press (1988)). Among these, viral diseases constitute a major hindrance to profitable growing of grapevines. About 34 viruses have been isolated and characterized from grapevines. The major virus diseases are grouped into: (1) the grapevine degeneration caused by the fanleaf nepovirus, other European nepoviruses, and American nepoviruses, (2) the leafroll complex, and (3) the rugose wood complex (Martelli, ed., Graft Transmissible Diseases of Grapevines. Handbook for Detection and Diagnosis, FAO, UN, Rome, Italy (1993)).

Of the major virus diseases, the grapevine leafroll complex is the most widely distributed throughout the world. According to Goheen ("Grape Leafroll," in Frazier et al., eds., Virus Diseases of Small Fruits and Grapevines (A Handbook), University of California, Division of Agricultural Sciences, Berkeley, Calif, USA, pp. 209-212 (1970) ("Goheen (1970)"), grapevine leafroll-like disease was described as early as the 1850s in German and French literature. However, the viral nature of the disease was first demonstrated by Scheu (Scheu, "Die Rollkrankheit des Rebstockes (Leafroll of grapevine)," D. D. Weinbau 14:222-358 (1935) ("Scheu (1935)")). In 1946, Harmon and Snyder (Harmon et al., "Investigations on the Occurrence, Transmission, Spread and Effect of 'White' Fruit Colour in the Emperor Grape," Proc. Am. Soc. Hort. Sci. 74:190-194 (1946)) determined the viral nature of White Emperor disease in California. It was later proven by Goheen et al. (Goheen et al., "Leafroll (White Emperor Disease) of Grapes in California," Phytopathology, 48:51-54 (1958) ("Goheen (1958)")) that both leafroll and "White Emperor" diseases were the same, and only the name "leafroll" was retained.

Leafroll is a serious viral disease of grapes and occurs wherever grapes are grown. This wide distribution of the disease has come about through the propagation of diseased vines. It affects almost all cultivated and rootstock varieties of *Vitis*. Although the disease is not lethal, it causes yield losses and reduction of sugar content. Scheu estimated in 1936 that 80 per cent of all grapevines planted in Germany were infected (Scheu, Mein Winzerbuch, Berlin:Reichsnährstand-Verlags (1936)). In many California wine grape vineyards, the incidence of leafroll (based on a survey of field symptoms conducted in 1959) agrees with Scheu's initial observation in German vineyards (Goheen et al., "Studies of Grape Leafroll in California," Amer. J. Enol. Vitic., 10:78-84 (1959)). The current situation on leafroll disease does not seem to be any better (Goheen, "Diseases Caused by Viruses and Viruslike Agents," The American Phytopathological Society, St. Paul, Minnesota:APS Press, 1:47-54 (1988) ("Goheen (1988)")). Goheen also estimated that the disease causes an annual loss of about 5-20 per cent of the total grape production (Goheen (1970) and Goheen (1988)).

The amount of sugar in individual berries of infected vines is only about 1/2 to 2/3 that of berries from noninfected vines (Goheen (1958)).

Symptoms of leafroll disease vary considerably depending upon the cultivar, environment, and time of the year. On red or dark-colored fruit varieties, the typical
 5 downward rolling and interveinal reddening of basal, mature leaves is the most prevalent in autumn; but not in spring or early summer. On light-colored fruit varieties however, symptoms are less conspicuous, usually with downward rolling accompanied by interveinal chlorosis. Moreover, many infected rootstock cultivars do not develop symptoms. In these cases, the disease is usually diagnosed with a woody indicator indexing assay using *Vitis*
 10 *vivifera* cv. Carbernet Franc (Goheen (1988)).

Ever since Scheu demonstrated that leafroll was graft transmissible, a virus etiology has been suspected (Scheu (1935)). Several virus particle types have been isolated from leafroll diseased vines. These include potyvirus-like (Tanne et al., "Purification and Characterization of a Virus Associated with the Grapevine Leafroll Disease,"
 15 Phytopathology, 67:442-447 (1977)), isometric virus-like (Castellano et al., "Virus-like Particles and Ultrastructural Modifications in the Phloem of Leafroll-affected Grapevines," Vitis, 22:23-39 (1983) ("Castellano (1983)")) and Namba et al., "A Small Spherical Virus Associated with the Ajinashika Disease of Koshu Grapevine, Ann. Phytopathol. Soc. Japan, 45:70-73 (1979)), and closterovirus-like (Namba, "Grapevine Leafroll Virus, a Possible
 20 Member of Closteroviruses, Ann. Phytopathol. Soc. Japan, 45:497-502 (1979)) particles. In recent years, however, long flexuous closteroviruses ranging from 1,400 to 2,200 nm have been most consistently associated with leafroll disease (Figure 1) (Castellano (1983), Faoro et al., "Association of a Possible Closterovirus with Grapevine Leafroll in Northern Italy," Riv. Patol. Veg., Ser IV, 17:183-189 (1981), Gugerli et al., "L'enroulement de la vigne: mise
 25 en évidence de particules virales et développement d'une méthode immuno-enzymatique pour le diagnostic rapide (Grapevine Leafroll: Presence of Virus Particles and Development of an Immuno-enzyme method for Diagnosis and Detection)," Rev. Suisse Viticult. Arboricult. Hort., 16:299-304 (1984) ("Gugerli (1984)"), Hu et al., "Characterization of Closterovirus-like Particles Associated with Grapevine Leafroll Disease," J. Phytopathol.,
 30 128:1-14 (1990) ("Hu (1990)"), Milne et al., "Closterovirus-like Particles of Two Types Associated with Diseased Grapevines," Phytopathol. Z., 110:360-368 (1984), Zee et al., "Cytopathology of Leafroll-diseased Grapevines and the Purification and Serology of Associated Closteroviruslike Particles," Phytopathology, 77:1427-1434 (1987) ("Zee (1987)"), and Zimmermann et al., "Characterization and Serological Detection of Four

Closterovirus-like Particles Associated with Leafroll Disease on Grapevine,” J. Phytopathol., 130:205-218 (1990) (“Zimmermann (1990)”). These closteroviruses are referred to as grapevine leafroll associated viruses (“GLRaV”). At least six serologically distinct types of GLRaV’s (GLRaV-1 to -6) have been detected from leafroll diseased vines (Table 1) (Boscia et al., “Nomenclature of Grapevine Leafroll-associated Putative Closteroviruses, Vitis, 34:171-175 (1995) (“Boscia (1995)”) and (Martelli, “Leafroll,” pp. 37-44 in Martelli, ed., Graft Transmissible Diseases of Grapevines, Handbook for Detection and Diagnosis, FAO, Rome Italy, (1993) (“Martelli I”). The first five of these were confirmed in the 10th Meeting of the International Council for the Study of Virus and Virus Diseases of the Grapevine (“ICVG”) (Volos, Greece, 1990).

TABLE 1

Type	Particle length (nm)	Coat protein <i>Mr</i> (X10 ³)	Reference
GLRaV-1	1,400-2,200	39	Gugerli (1984)
GLRaV-2	1,400-1,800	26	Gugerli (1984) Zimmermann (1990)
GLRaV-3	1,400-2,200	43	Zee (1987)
GLRaV-4	1,400-2,200	36	Hu (1990)
GLRaV-5	1,400-2,200	36	Zimmermann (1990)
GLRaV-6	1,400-2,200	36	Gugerli (1993)

Through the use of monoclonal antibodies, however, the original GLRaV II described in Gugerli (1984) has been shown to be an apparent mixture of at least two components, IIa and IIb (Gugerli et al., “Grapevine Leafroll Associated Virus II Analyzed by Monoclonal Antibodies,” 11th Meeting of the International Council for the Study of Viruses and Virus Diseases of the Grapevine, Montreux, Switzerland, pp. 23-24 (1993) (“Gugerli (1993)”). Recent investigation with comparative serological assays (Boscia (1995)) demonstrated that the IIb component of cv. Chasselas 8/22 is the same as the GLRaV-2 isolate from France (Zimmermann (1990)) which also include the isolates of grapevine corky bark associated closteroviruses from Italy (GCBaV-BA) (Boscia (1995)) and from the United States

(GCBaV-NY) (Namba et al., "Purification and Properties of Closterovirus-like Particles Associated with Grapevine Corky Bark Disease," Phytopathology, 81:964-970 (1991) ("Namba (1991)")). The IIa component of cv. Chasselas 8/22 was given the provisional name of grapevine leafroll associated virus 6 (GLRaV-6). Furthermore, the antiserum to the CA-5 isolate of GLRaV-2 produced by Boscia et al. (Boscia et al., "Characterization of Grape Leafroll Associated Closterovirus (GLRaV) Serotype II and Comparison with GLRaV Serotype III," Phytopathology, 80:117 (1990)) was shown to contain antibodies to both GLRaV-2 and GLRaV-1, with a prevalence of the latter (Boscia (1995)).

Virions of GLRaV-2 are flexuous, filamentous particles about 1,400-1,800 nm in length (Gugerli et al., "L'enroulement de la Vigne: Mise en Evidence de Particles Virales et Development d'une Methode Immuno-enzymatique Pour le Diagnostic Rapide (Grapevine Leafroll: Presence of Virus Particles and Development of an Immuno-enzyme Method for Diagnosis and Detection)," Rev. Suisse Viticult. Arboricult. Hortic. 16:299-304 (1984)). A double-stranded RNA (dsRNA) of about 15 kb was consistently isolated from GLRaV-2 infected tissues (Goszczynski et al., "Detection of Two Strains of Grapevine Leafroll-Associated Virus 2," Vitis 35:133-35 (1996)). The coat protein of GLRaV-2 is ca 22~26 kDa (Zimmermann et al., "Characterization and Serological Detection of Four Closterovirus-like Particles Associated with Leafroll Disease on Grapevine," J. Phytopathology 130:205-18 (1990); Gugerli and Ramel, Extended abstracts: "Grapevine Leafroll Associated Virus II Analyzed by Monoclonal Antibodies," 11th ICVG at Montreux, Switzerland, Gugerli, ed., Federal Agricultural Research Station of Changins, CH-1260 Nyon, Switzerland, p. 23-24 (1993); Boscia et al., "Nomenclature of Grapevine Leafroll-Associated Putative Closteroviruses," Vitis 34:171-75 (1995)), which is considerably smaller than other GLRaVs (35~43 kDa) (Zee et al., "Cytopathology of Leafroll-Diseased Grapevines and the Purification and Serology of Associated Closterovirus Like Particles," Phytopathology 77:1427-34 (1987); Hu et al., "Characterization of Closterovirus-Like Particles Associated with Grapevine Leafroll Disease," J. of Phytopathology 128:1-14 (1990); Ling et al., "The Coat Protein Gene of Grapevine Leafroll Associated Closterovirus-3: Cloning, Nucleotide Sequencing and Expression in Transgenic Plants," Arch. of Virology 142:1101-16 (1997)). Although GLRaV-2 has been classified as a member of the genus *Closterovirus* based on particle morphology and cytopathology (Martelli, Circular of ICTV-Plant Virus Subcommittee Study Group on Closterolike Viruses" (1996)), its molecular and biochemical properties are not well characterized.

In the closterovirus group, several viruses have recently been sequenced. The partial or complete genome sequences of beet yellows virus (BYV) (Agranovsky et al. "Nucleotide Sequence of the 3'-Terminal Half of Beet Yellows Closterovirus RNA Genome Unique Arrangement of Eight Virus Genes," J. General Virology 72:15-24 (1991);

5 Agranovsky et al., "Beet Yellows Closterovirus: Complete Genome Structure and Identification of a Papain-like Thiol Protease," Virology 198:311-24 (1994)), beet yellow stunt virus (BYSV) (Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses," Virology 221:199-207 (1996)), citrus tristeza virus (CTV) (Pappu et al., "Nucleotide Sequence and

10 Organization of Eight 3' Open Reading Frames of the Citrus Tristeza Closterovirus Genome," Virology 199:35-46 (1994); Karasev et al., "Complete Sequence of the Citrus Tristeza Virus RNA Genome," Virology 208:511-20 (1995)), lettuce infectious yellows virus (LIYV) (Klaassen et al., "Partial Characterization of the Lettuce Infectious Yellows Virus Genomic RNAs, Identification of the Coat Protein Gene and Comparison of its Amino Acid Sequence

15 With Those of Other Filamentous RNA Plant Viruses," J. General Virology 75:1525-33 (1994); Klaassen et al., "Genome Structure and Phylogenetic Analysis of Lettuce Infectious Yellows Virus, a Whitefly-Transmitted, Bipartite Closterovirus," Virology 208:99-110 (1995)), little cherry virus (LChV) (Keim and Jelkmann, "Genome Analysis of the 3'-Terminal Part of the Little Cherry Disease Associated dsRNA Reveals a Monopartite

20 Closterovirus-Like Virus," Arch. Virology 141:1437-51 (1996); Jelkmann et al., "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus," J. General Virology 78:2067-71 (1997)), and GLRaV-3 (Ling et al., "Nucleotide Sequence of the 3' Terminal Two-Thirds of the Grapevine Leafroll Associated Virus-3 Genome Reveals a Typical Monopartite Closterovirus," J. Gen. Virology

25 79(5):1289-1301 (1998)) revealed several common features of the closteroviruses, including the presence of HSP70 chaperone heat shock protein and a duplicate of the coat protein gene (Agranovsky "Principles of Molecular Organization, Expression, and Evolution of Closteroviruses: Over the Barriers," Adv. in Virus Res. 47:119-218 (1996); Dolja et al. "Molecular Biology and Evolution of Closteroviruses: Sophisticated Build-up of Large RNA

30 Genomes," Annual Rev. Photopathology 32:261-85 (1994); Boyko et al., "Coat Protein Gene Duplication in a Filamentous RNA Virus of Plants," Proc. Nat. Acad. Sci. USA 89:9156-60 (1992)). Characterization of the genome organization of GLRaVs would provide molecular information on the serologically distinct closteroviruses that cause similar leafroll symptoms in grapevine.

Several shorter closteroviruses (particle length 800 nm long) have also been isolated from grapevines. One of these, called grapevine virus A ("GVA") has also been found associated, though inconsistently, with the leafroll disease (Agran et al., "Occurrence of Grapevine Virus A (GVA) and Other Closteroviruses in Tunisian Grapevines Affected by Leafroll Disease," Vitis, 29:43-48 (1990), Conti, et al., "Closterovirus Associated with Leafroll and Stem Pitting in Grapevine," Phytopathol. Mediterr., 24:110-113 (1985), and Conti et al., "A Closterovirus from a Stem-pitting-diseased Grapevine," Phytopathology, 70:394-399 (1980)). The etiology of GVA is not really known; however, it appears to be more consistently associated with rugose wood *sensu lato* (Rosciglione et al., "Maladies de l'enroulement et du bois strié de la vigne: analyse microscopique et sérologique (Leafroll and Stem Pitting of Grapevine: Microscopical and Serological Analysis)," Rev. Suisse Vitic Arboric. Hortic., 18:207-211 (1986) ("Rosciglione (1986)"), and Zimmermann (1990)). Moreover, another short closterovirus (800 nm long) named grapevine virus B ("GVB") has been isolated and characterized from corky bark-affected vines (Boscia et al., "Properties of a Filamentous Virus Isolated from Grapevines Affected by Corky Bark," Arch. Virol., 130:109-120 (1993) and Namba (1991)).

As suggested by Martelli I, leafroll symptoms may be induced by more than one virus or they may be simply a general plant physiological response to invasion by an array of phloem-inhabiting viruses. Evidence accumulated in the last 15 years strongly favors the idea that grapevine leafroll is induced by one (or a complex) of long closteroviruses (particle length 1,400 to 2,200 nm).

Grapevine leafroll is transmitted primarily by contaminated scions and rootstocks. However, under field conditions, several species of mealybugs have been shown to be the vector of leafroll (Engelbrecht et al., "Transmission of Grapevine Leafroll Disease and Associated Closteroviruses by the Vine Mealybug *Planococcus ficus*," Phytophylactica, 22:341-346 (1990), Rosciglione, et al., "Transmission of Grapevine Leafroll Disease and an Associated Closterovirus to Healthy Grapevine by the Mealybug *Planococcus ficus*," (Abstract), Phytoparasitica, 17:63-63 (1989), and Tanne, "Evidence for the Transmission by Mealybugs to Healthy Grapevines of a Closter-like Particle Associated with Grapevine Leafroll Disease," Phytoparasitica, 16:288 (1988)). Natural spread of leafroll by insect vectors is rapid in various parts of the world. In New Zealand, observations of three vineyards showed that the number of infected vines nearly doubled in a single year (Jordan et al., "Spread of Grapevine Leafroll and its Associated Virus in New Zealand Vineyards," 11th Meeting of the International Council for the Study of Viruses and Virus Diseases of the

Grapevine, Montreux, Switzerland, pp. 113-114 (1993)). One vineyard became 90% infected 5 years after GLRaV-3 was first observed. Prevalence of leafroll worldwide may increase as chemical control of mealybugs becomes more difficult due to the unavailability of effective insecticides.

5 In view of the serious risk grapevine leafroll virus poses to vineyards and the absence of an effective treatment of it, the need to prevent this affliction continues to exist. The present invention is directed to overcoming this deficiency in the art.

SUMMARY OF INVENTION

10 The present invention relates to an isolated protein or polypeptide corresponding to a protein or polypeptide of a grapevine leafroll virus (type 2). The encoding RNA and DNA molecules, in either isolated form or incorporated in an expression system, a host cell, a transgenic *Vitis* or *citrus* scion or rootstock cultivar, or a transgenic *Nicotiana*
15 plant or beet plant are also disclosed.

Another aspect of the present invention relates to a method of imparting grapevine leafroll virus (type 2) resistance to *Vitis* scion or rootstock cultivars or *Nicotiana* plants by transforming them with a DNA molecule encoding the protein or polypeptide corresponding to a protein or polypeptide of a grapevine leafroll virus (type 2). Other aspects
20 of the present invention relate to a method of imparting beet yellows virus resistance to beet plants and a method of imparting tristeza virus resistance to citrus scion or rootstock cultivars, both by transforming the plants or cultivars with a DNA molecule encoding the protein or polypeptide corresponding to a protein or polypeptide of a grapevine leafroll virus (type 2).

25 The present invention also relates to an antibody or binding portion thereof or probe which recognizes the protein or polypeptide.

Grapevine leafroll virus resistant transgenic variants of the current commercial grape cultivars and rootstocks allows for more complete control of the virus, while retaining the varietal characteristics of specific cultivars. Furthermore, these variants permit control of
30 GLRaV-2 transmitted either by contaminated scions or rootstocks or by a presently uncharacterized insect vector. With respect to the latter mode of transmission, the present invention circumvents increased restriction of pesticide use which has made chemical control of insect infestation increasingly difficult. In this manner, the interests of the environment

and the economics of grape cultivation and wine making are all furthered by the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are a comparison of a double-stranded RNA (dsRNA) profile (Figure 1A) of GLRaV-2 and its Northern hybridization analysis (Figure 1B). In Figure 1A: lane M, lambda Hind III DNA marker; and lane 1, dsRNA pattern in 1% agarose gel stained with ethidium bromide. Figure 1B is a northern hybridization of isolated high molecular weight dsRNA of GLRaV-2 with a probe prepared with ^{32}P [α -dATP] labeled cDNA insert from GLRaV-2 specific cDNA clone TC-1. Lane 1, high molecular weight dsRNA of GLRaV-2. Lane 2, total RNA extracted from healthy grapevine.

Figure 2 displays the genome organization of GLRaV-2 and its sequencing strategy. Boxes represent ORFs encoded by deduced amino acid sequences of GLRaV-2, numbered lines represent nucleotide coordinates, beginning from 5'-terminal of RNA in kilobases (kb). The lines below GLRaV-2 RNA genome represent the cDNA clones used to determine the nucleotide sequences.

Figure 3A-3D are comparisons between ORF1a/ORF1b of GLRaV-2 and BYV. Figure 3A-3D show the conserved domains of two papain-like proteases (P-PRO), methyltransferase (MT/MTR), helicase (HEL), and RNA-dependent RNA polymerase (RdRP), respectively. Exclamation marks indicate the predicted catalytic residues of the leader papain-like protease; slashes indicate the predicted cleavage sites. The conserved motifs of the MT, HEL, and RdRP domains are highlighted with overlines marked with respective letters. The alignment is constructed using the MegAlign program in DNASTAR.

Figures 4A and 4B are alignments of the nucleotide (Figure 4A) and deduced amino acid (Figure 4B) sequences of ORF1a/ORF1b overlapping region of GLRaV-2, BYV, BYSV, and CTV. Identical nucleotides and amino acids are shown in consensus. GLRaV-2 putative + 1 frameshift site (TAGC) and its corresponding sites of BYV (TAGC) and BYSV (TAGC) and CTV (CGGC) at nucleotide and amino acid sequences are highlighted with underlines.

Figure 5 is an alignment of the amino acid sequence of HSP70 protein of GLRaV-2 and BYV. The conserved motifs (A to H) are indicated with overlines and marked

with respective letters. The alignment was conducted with the MegAlign program of DNASTAR.

Figure 6A is a comparison of the coat protein (CP) and coat protein duplicate (CPd) of GLRaV-2 with other closteroviruses. The amino acid sequence of the GLRaV-2 CP and CPd are aligned with the CP and CPd of BYV, BYSV, and CTV. The conserved amino acid residues are in bold and the consensus sequences are indicated. Sequence alignment and phylogenetic tree were constructed by Clustal Method in the MegAlign Program of DNASTAR. Figure 6B is a tentative phylogenetic tree of the CP and CPd of GLRaV-2 with BYV, BYSV, CTV, LIYV, LChV, and GLRaV-3. To facilitate the alignment, only the C-terminal 250 amino acids of CP and CPd of LIYV, LChV, and GLRaV-3 were used. The scale beneath the phylogenetic tree represents the distance between sequences. Units indicate the number of substitution events.

Figure 7 is a comparison of the genome organization of GLRaV-2, BYV, BYSV, CTV, LIYV, LChV, and GLRaV-3. P-PRO, papain-like protease; MT/MTR, methyltransferase; HEL, helicase; RdRP, RNA-dependent RNA polymerase; HSP70, heat shock protein 70; CP, coat protein; CPd, coat protein duplicate.

Figure 8 is a tentative phylogenetic tree showing the relationship of RdRP of GLRaV-2 with respect to BYV, BYSV, CTV, and LIYV. The phylogenetic tree was constructed using the Clustal method with the MegAlign program in DNASTAR.

Figure 9 is an alignment of the amino acid sequence of HSP90 protein of GLRaV-2 with respect to other closteroviruses, BYV, BYSV, and CTV. The most conserved motifs (I to II) are indicated with the highlighted lines and marked with respective letters.

Figure 10 is an alignment of the nucleotide sequence of 3'-terminal untranslated region of GLRaV-2 with respect to the closteroviruses BYV (Agranovsky et al., "Beet Yellows Closterovirus: Complete Genome Structure and Identification of a Papain-like Thiol Protease," *Virology* 198:311-24 (1994), which is hereby incorporated by reference), BYSV (Karasev et al., Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses," *Virology* 221:199-207 (1996), which is hereby incorporated by reference), and CTV (Karasev et al., "Complete Sequence of the Citrus Tristeza Virus RNA Genome," *Virology* 208:511-20 (1995), which is hereby incorporated by reference). The consensus sequences are shown, and the distance to the 3'-end is indicated. A complementary region capable of forming a "hair-pin" structure is underlined.

Figures 11A and 11B are genetic maps of the transformation vectors

pGA482GG/EPT8CP-GLRaV-2 and pGA482G/EPT8CP-GLRaV-2, respectively. As shown in Figures 11A and 11B, the plant expression cassette (EPT8CP-GLRaV-2), which consists of a double cauliflower mosaic virus (CaMV) 35S-enhancer, a CaMV 35S-promoter, an alfalfa mosaic virus (ALMV) RNA4 5' leader sequence, a coat protein gene of GLRaV-2 (CP-GLRaV-2), and a CaMV 35S 3' untranslated region as a terminator, was cloned into the transformation vector by EcoR I restriction site. The CP of GLRaV-2 was cloned into the plant expression vector by Nco I restriction site.

Figure 12 is a PCR analysis of DNA molecules extracted from the leaves of putative transgenic plants using both the CP gene of GLRaV-2 and NPT II gene specific primers. An ethidium bromide-stained gel shows a 720 bp amplified DNA fragment for NPT II gene, and a 653 bp DNA fragment for the entire coding sequence of the CP gene. Lane 1, Φ 174 / Hae III DNA Marker; lanes 2-6, transgenic plants from different lines; lane 7, the cp gene of GLRaV-2 of positive control; and lane 8, NPT II gene of positive control.

Figure 13 is a comparison of resistant (right side 3 plants) and susceptible (left side 3 plants) transgenic *Nicotiana benthamiana* plants. Plants are shown 48 days after inoculation with GLRaV-2.

Figure 14 is a northern blot analysis of transgenic *Nicotiana benthamiana* plants. An aliquot of 10 g of total RNA extracted from putative transgenic plants was denatured and loaded onto 1% agarose gel containing formaldehyde. The separated RNAs were transferred to Gene Screen Plus membrane and hybridized with a 32 P-labeled DNA probe containing the 3' one third CP gene sequence. Lanes 1, 3, and 4 represent nontransformed control plants without RNA expression. The remaining lanes represent transgenic plants from different lines: lanes 2, 14-17, and 22-27 represent plants with high RNA expression level which are susceptible to GLRaV-2; all other lanes represent plants with undetectable or low RNA expression level which are resistant to GLRaV-2.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to isolated DNA molecules encoding for the proteins or polypeptides of a grapevine leafroll virus (type 2). A substantial portion of the grapevine leafroll virus (type-2) ("GLRaV-2") genome has been sequenced. Within the genome are a plurality of open reading frames ("ORFs") and a 3' untranscribed region ("UTR"), each containing DNA molecules in accordance with the present invention. The

DNA molecule which constitutes a substantial portion of the GLRaV-2 genome comprises the nucleotide sequence corresponding to SEQ. ID. No. 1 as follows:

TAAACATTGC	GAGAGAACCC	CATTAGCGTC	TCCGGGGTGA	ACTTGGGAAG	GTCTGCCGCC	60
GCTCAGGTTA	TTTATTTTCG	CAGTTTCACG	CAGCCCTTCG	CGTTGTATCC	GCGCCAAGAG	120
AGCGCGATCG	TAAAAACGCA	ACTTCCACCG	GTCAGTGTAG	TGAAGGTGGA	GTGCGTAGCT	180
GCGGAGGTAG	CTCCCGACAG	GGGCGTGGTC	GACAAGAAAC	CTACGTCTGT	TGGCGTTCCC	240
CCGCAGCGCG	GTGTGCTTTC	TTTTCCGACG	GTGGTTCGGA	ACCGCGGCGA	CGTGATAATC	300
ACAGGGGTGG	TGCATGAAGC	CCTGAAGAAA	ATTAAAGACG	GGCTCTTACG	CTTCCGCGTA	360
GGCGGTGACA	TGCGTTTTTC	GAGATTTTTC	TCATCGAACT	ACGGCTGCAG	ATTCGTCGCG	420
AGCGTGCGTA	CGAACACTAC	AGTTTGGCTA	AATTGCACGA	AAGCGAGTGG	TGAGAAATTC	480
TCACTCGCCG	CCGCGTGCAC	GGCGGATTAC	GTGGCGATGC	TGCGTTATGT	GTGTGGCGGG	540
AAATTTCCAC	TCGTCCTCAT	GAGTAGAGTT	ATTTACCCGG	ATGGGCGCTG	TTACTTGGCC	600
CATATGAGGT	ATTTGTGCGC	CTTTTACTGT	CGCCCGTTTA	GAGAGTCGGA	TTATGCCCTC	660
GGAATGTGGC	CTACGGTGGC	GCGTCTCAGG	GCATGCGTTG	AGAAGAACTT	CGGTGTCGAA	720
GCTTGTGGCA	TAGCTCTTCG	TGGCTATTAC	ACCTCTCGCA	ATGTTTATCA	CTGTGATTAT	780
GACTCTGCTT	ATGTAAAATA	TTTGTAGAAC	CTTTCCGGCC	GCATTGGCGG	TGGTTCGTTC	840
GATCCGACAT	CTTTAACCTC	CGTAATAACG	GTGAAGATTA	GCGGTCTTCC	AGGTGGTCTT	900
CCTAAAAATA	TAGCGTTTGG	TGCCTTCCTG	TGCGATATAC	GTTACGTCGA	ACCGGTAGAC	960
TCGGGCGGCA	TTCAATCGAG	CGTTAAGACG	AAACGTGAAG	ATGCGCACCG	AACCGTAGAG	1020
GAACGGGCGG	CCGGCGGATC	CGTCGAGCAA	CCGCGACAAA	AGAGGATAGA	TGAGAAAGGT	1080
TGCGGCAGAG	TTCTTAGTGG	AGGTTTTTTC	CATCTCCTGG	TCGGCAACCT	TAACGAAGTT	1140
AGGAGGAAGG	TAGCTGCCGG	ACTTCTACGC	TTTCGCGTTG	GCGGTGATAT	GGATTTTCAT	1200
CGCTCGTTCT	CCACCCAAGC	GGGCCACCGC	TTGCTGGTGT	GGCGCCGCTC	GAGCCGGAGC	1260
GTGTGCCTTG	AACTTTACTC	ACCATCTAAA	AACTTTTTGC	GTTACGATGT	CTTGCCCTGT	1320
TCTGGAGACT	ATGCAGCGAT	GTTTTCTTTC	GCGGCGGGCG	GCCGTTTCCC	TTTAGTTTTG	1380
ATGACTAGAA	TTAGATACCC	GAACGGGTTT	TGTTACTTGG	CTCACTGCCG	GTACGCGTGC	1440
GCGTTTCTCT	TAAGGGGTTT	TGATCCGAAG	CGTTTCGACA	TCGGTGCTTT	CCCACCGCG	1500
GCCAAGCTCA	GAAACCGTAT	GGTTTCGGAG	CTTGGTGAAA	GAAGTTTAGG	TTTGAACCTG	1560
TACGGCGCAT	ATACGTCACG	CGGCGTCTTT	CACTGCGATT	ATGACGCTAA	GTTTATAAAG	1620
GATTTGCGTC	TTATGTCAGC	AGTTATAGCT	GGAAAGGACG	GGGTGGAAGA	GGTGGTACCT	1680

TCTGACATAA CTCCTGCCAT GAAGCAGAAA ACGATCGAAG CCGTGTATGA TAGATTATAT	1740
GGCGGCACTG ACTCGTTGCT GAAACTGAGC ATCGAGAAAG ACTTAATCGA TTTCAAAAAT	1800
GACGTGCAGA GTTTGAAGAA AGATCGGCCG ATTGTCAAAG TGCCCTTTTA CATGTCGGAA	1860
GCAACACAGA ATTCGCTGAC GCGTTTCTAC CCTCAGTTCG AACTTAAGTT TTCGCACTCC	1920
TCGCATTAG ATCATCCCGC CGCCGCCGCT TCTAGACTGC TGGAAAATGA AACGTTAGTG	1980
CGCTTATGTG GTAATAGCGT TTCAGATATT GGAGGTTGTC CTCTTTTCCA TTTGCATTCC	2040
AAGACGCAAA GACGGGTTCA CGTATGTAGG CCTGTGTTGG ATGGCAAGGA TGCGCAGCGT	2100
CGCGTGGTGC GTGATTTGCA GTATTCCAAC GTGCGTTTGG GAGACGATGA TAAAATTTTG	2160
GAAGGGCCAC GCAATATCGA CATTTGCCAC TATCCTCTGG GCGCGTGTGA CCACGAAAGT	2220
AGTGCTATGA TGATGGTGCA GGTGTATGAC GCGTCCCTTT ATGAGATATG TGGCGCCATG	2280
ATCAAGAAGA AAAGCCGCAT AACGTACTTA ACCATGGTCA CGCCCGGCCA GTTCTTGAC	2340
GGACGCGAAT GCGTCTACAT GGAGTCGTTA GACTGTGAGA TTGAAGTTGA TGTGCACGCG	2400
GACGTCGTAA TGTACAAATT CGGTAGTTCT TGCTATTGCG ACAAGCTTTC AATCATCAAG	2460
GACATCATGA CCACTCCGTA CTTGACACTA GGTGGTTTTT TATTAGCGT GGAGATGTAT	2520
GAGGTGCGTA TGGGCGTGAA TTACTTCAAG ATTACGAAGT CCGAAGTATC GCCTAGCATT	2580
AGCTGCACCA AGCTCCTGAG ATACCGAAGA GCTAATAGTG ACGTGGTTAA AGTTAAACTT	2640
CCACGTTTTG ATAAGAAACG TCGCATGTGT CTGCCTGGGT ATGACACCAT ATACCTAGAT	2700
TCGAAGTTTG TGAGTCGCGT TTTCGATTAT GTCGTGTGTA ATTGCTCTGC CGTGAACCTCA	2760
AAAACTTTCG AGTGGGTGTG GAGTTTCATT AAGTCTAGTA AGTCGAGGGT GATTATTAGC	2820
GGTAAAATAA TTCACAAGGA TGTGAATTTG GACCTCAAGT ACGTCGAGAG TTTCGCCGCG	2880
GTTATGTTGG CCTCTGGCGT GCGCAGTAGA CTAGCGTCCG AGTACCTTGC TAAGAACCTT	2940
AGTCATTTTT CGGGAGATTG CTCCTTTATT GAAGCCACGT CTTTCGTGTT GCGTGAGAAA	3000
ATCAGAAACA TGAATCTGAA TTTTAACGAA AGACTTTTAC AGTTAGTGAA GCGCGTTGCC	3060
TTTGCGACCT TGGACGTGAG TTTTCTAGAT TTAGATTCAA CTCTTGAATC AATAACTGAT	3120
TTTGCCGAGT GTAAGGTAGC GATTGAACTC GACGAGTTGG GTTGCTTGAG AGCGGAGGCC	3180
GAGAATGAAA AAATCAGGAA TCTGGCGGGA GATTCGATTG CGGCTAAACT CGCGAGCGAG	3240
ATAGTGGTCG ATATTGACTC TAAGCCTTCA CCGAAGCAGG TGGGTAATTC GTCATCCGAA	3300
AACGCCGATA AGCGGGAAGT TCAGAGGCCC GGTGTCGTG GTGGTTCTAG AAACGGGGTT	3360
GTTGGGGAGT TCCTTCACTT CGTCGTGGAT TCTGCCCTGC GTCTTTTCAA ATACGCGACG	3420
GATCAACAAC GGATCAAGTC TTACGTGCGT TTCTTGGACT CGGCGGTCTC ATTCTTGGAT	3480
TACAACACG ATAATCTATC GTTTATACTG CGAGTGCTTT CGGAAGGTTA TTCGTGTATG	3540

TTCGCGTTTT	TGGCGAATCG	CGGCGACTTA	TCTAGTCGTG	TCCGTAGCGC	GGTGTGTGCT	3600
GTGAAAGAAG	TTGCTACCTC	ATGCGCGAAC	GCGAGCGTTT	CTAAAGCCAA	GGTTATGATT	3660
ACCTTCGCAG	CGGCCGTGTG	TGCTATGATG	TTTAATAGCT	GCGGTTTTTC	AGGCGACGGT	3720
CGGGAGTATA	AATCGTATAT	ACATCGTTAC	ACGCAAGTAT	TGTTTGACAC	TATCTTTTTT	3780
GAGGACAGCA	GTTACCTACC	CATAGAAGTT	CTGAGTTCGG	CGATATGCGG	TGCTATCGTC	3840
ACACTTTTCT	CCTCGGGCTC	GTCCATAAGT	TTAAACGCCT	TCTTACTTCA	AATTACCAAA	3900
GGATTCTCCC	TAGAGGTTGT	CGTCCGGAAT	GTTGTGCGAG	TCACGCATGG	TTTGAGCACC	3960
ACAGCGACCG	ACGGCGTCAT	ACGTGGGGTT	TTCTCCCAA	TTGTGTCTCA	CTTACTTGTT	4020
GGAAATACGG	GTAATGTGGC	TTACCAGTCA	GCTTTCATTG	CCGGGGTGGT	GCCTCTTTTA	4080
GTTAAAAAGT	GTGTGAGCTT	AATCTTCATC	TTGCGTGAAG	ATACTTATTC	CGGTTTTATT	4140
AAGCACGGAA	TCAGTGAATT	CTCTTTCCTT	AGTAGTATTC	TGAAGTTCTT	GAAGGGTAAG	4200
CTTGTTGGACG	AGTTGAAATC	GATTATTCAA	GGGGTTTTTG	ATTCCAACAA	GCACGTGTTT	4260
AAAGAAGCTA	CTCAGGAAGC	GATTTCGTACG	ACGGTCATGC	AAGTGCCTGT	CGCTGTAGTG	4320
GATGCCCTTA	AGAGCGCCGC	GGGAAAATT	TATAACAATT	TTACTAGTCG	ACGTACCTTT	4380
GGTAAGGATG	AAGGCTCCTC	TAGCGACGGC	GCATGTGAAG	AGTATTTCTC	ATGCGACGAA	4440
GGTGAAGGTC	CGGGTCTGAA	AGGGGGTTCC	AGCTATGGCT	TCTCAATTTT	AGCGTTCTTT	4500
TCACGCATTA	TGTGGGGAGC	TCGTGGGCTT	ATTGTTAAGG	TGAAGCATGA	GTGTTTTGGG	4560
AAACTTTTTG	AATTTCTATC	GCTCAAGCTT	CACGAATTCA	GGACTCGCGT	TTTTGGGAAG	4620
AATAGAACGG	ACGTGGGAGT	TTACGATTTT	TTGCCACGG	GCATCGTGGA	AACGCTCTCA	4680
TCGATAGAAG	AGTGCGACCA	AATTGAAGAA	CTTCTCGGCG	ACGACCTGAA	AGGTGACAAG	4740
GATGCTTCGT	TGACCGATAT	GAATTACTTT	GAGTTCTCAG	AAGACTTCTT	AGCCTCTATC	4800
GAGGAGCCGC	CTTTCGCTGG	ATTGCGAGGA	GGTAGCAAGA	ACATCGCGAT	TTTGCGGATT	4860
TTGGAATACG	CGCATAATTT	GTTTCGCATT	GTCGCAAGCA	AGTGTTGAA	ACGACCTTTA	4920
TTTCTTGCTT	TCGCCGAAT	CTCAAGCGCC	CTTATCGAGA	AATTTAAGGA	GGTTTTCCCT	4980
CGTAAGAGCC	AGCTCGTCGC	TATCGTGCGC	GAGTATACTC	AGAGATTCTT	CCGAAGTCGC	5040
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GCATTAATGA	AGCGGAAGGT	TTCAGGTTTC	TTCTTAGCTA	GTGTTTATCG	CCCACTTAGA	5160
GGTTTCTCAT	ATATGTGTGT	TTCAGCGGAG	CGACGTGAAA	AGTTTTTTGC	TCTCGTGTGT	5220
TTAATCGGGT	TAAGTCTCCC	TTTCTTCGTG	CGCATCGTAG	GAGCGAAAGC	GTGCGAAGAA	5280
CTCGTGTCTT	CAGCGCGTCG	CTTTTATGAG	CGTATTAAAA	TTTTTCTAAG	GCAGAAGTAT	5340

GTCTCTCTTT	CTAATTTCTT	TTGTCACCTG	TTTAGCTCTG	ACGTTGATGA	CAGTTCCGCA	5400
TCTGCAGGGT	TGAAAGGTGG	TGCGTCGCGA	ATGACGCTCT	TCCACCTTCT	GGTTCGCCTT	5460
GCTAGTGCCC	TCCTATCGTT	AGGGTGGGAA	GGGTAAAGC	TACTCTTATC	GCACCACAAC	5520
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GGTCTTTCTT	TCTTTGTGCA	ACCAATCTTT	TCCTTGTTTG	CGGCGATGCT	TCTACAACCG	5640
GACAGGTTTG	TGGAGTATTC	CGAGAAACTT	GTTACAGCGT	TTGAATTTTT	CTTAAAAATG	5700
TCGCCTCGCG	CGCCTGCACT	ACTCAAAGGG	TTTTTTGAGT	GCGTGGCGAA	CAGCACTGTG	5760
TCAAAAACCG	TTCGAAGACT	TCTTCGCTGT	TTCGTGAAGA	TGCTCAAAC	TCGAAAAGGG	5820
CGAGGGTTGC	GTGCGGATGG	TAGGGGTCTC	CATCGGCAGA	AAGCCGTACC	CGTCATACCT	5880
TCTAATCGGG	TCGTGACCGA	CGGGGTTGAA	AGACTTTCGG	TAAAGATGCA	AGGAGTTGAA	5940
GCGTTGCGTA	CCGAATTGAG	AATCTTAGAA	GATTTAGATT	CTGCCGTGAT	CGAAAAACTC	6000
AATAGACGCA	GAAATCGTGA	CACTAATGAC	GACGAATTTA	CGCGCCCTGC	TCATGAGCAG	6060
ATGCAAGAAG	TCACCACTTT	CTGTTCGAAA	GCCAACTCTG	CTGGTTTGGC	CCTGGAAAGG	6120
GCAGTGCTTG	TGGAAGACGC	TATAAAGTCG	GAGAACTTT	CTAAGACGGT	TAATGAGATG	6180
GTGAGGAAAG	GGAGTACCAC	CAGCGAAGAA	GTGGCCGTGC	CTTTGTCGGA	CGATGAAGCC	6240
GTGGAAGAAA	TCTCTGTTGC	TGACGAGCGA	GACGATTCGC	CTAAGACAGT	CAGGATAAGC	6300
GAATACCTAA	ATAGGTTAAA	CTCAAGCTTC	GAATTCCCGA	AGCCTATTGT	TGTGGACGAC	6360
AACAAGGATA	CCGGGGGTCT	AACGAACGCC	GTGAGGGAGT	TTTATTATAT	GCAAGAACTT	6420
GCTCTTTTCG	AAATCCACAG	CAAACGTGTC	ACCTACTACG	ATCAACTGCG	CATAGTCAAC	6480
TTCGATCGTT	CCGTAGCACC	ATGCAGCGAA	GATGCTCAGC	TGTACGTACG	GAAGAACGGC	6540
TCAACGATAG	TGCAGGGTAA	AGAGGTACGT	TTGCACATTA	AGGATTTCCA	CGATCACGAT	6600
TTCTGTTTG	ACGGAAAAAT	TTCTATTAAC	AAGCGCGGC	GAGGCGGAAA	TGTTTTATAT	6660
CACGACAACC	TCGCGTTCTT	GGCGAGTAAT	TTGTTCTTAG	CCGGCTACCC	CTTTTCAAGG	6720
AGCTTCGTCT	TCACGAATTC	GTCGGTCGAT	ATTCTCCTCT	ACGAAGCTCC	ACCCGGAGGT	6780
GGTAAGACGA	CGACGCTGAT	TGACTCGTTC	TTGAAGGTCT	TCAAGAAAGG	TGAGGTTTCC	6840
ACCATGATCT	TAACCGCCAA	CAAAAGTTCG	CAGGTTGAGA	TCCTAAAGAA	AGTGGAGAAG	6900
GAAGTGCTTA	ACATTGAATG	CCAGAAACGT	AAAGACAAAA	GATCTCCGAA	AAAGAGCATT	6960
TACACCATCG	ACGCTTATTT	AATGCATCAC	CGTGGTTGTG	ATGCAGACGT	TCTTTTCATC	7020
GATGAGTGTT	TCATGGTTCA	TGCGGGTAGC	GTAAGCTT	GCATTGAGTT	CACGAGGTGT	7080
CATAAAGTAA	TGATCTTCGG	GGATAGCCGG	CAGATTCACT	ACATTGAAAG	GAACGAATTG	7140
GACAAGTGTT	TGTATGGGGA	TCTCGACAGG	TTCGTGGACC	TGCAGTGTGC	GGTTTATGGT	7200

AATATTTTCGT	ACCGTTGTCC	ATGGGATGTG	TGCGCTTGGT	TAAGCACAGT	GTATGGCAAC	7260
CTAATCGCCA	CCGTGAAGGG	TGAAAGCGAA	GGTAAGAGCA	GCATGCGCAT	TAACGAAATT	7320
AATTCAGTCG	ACGATTTAGT	CCCCGACGTG	GGTTCCACGT	TTCTGTGTAT	GCTTCAGTCG	7380
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ACGGTG CATG	AGGCGCAAGG	TGAGACGTAT	GCGCGTGTGA	ACCTTGTGCG	ACTTAAGTTT	7500
CAGGAGGATG	AACCCTTTAA	ATCTATCAGG	CACATAACCG	TCGCTCTTTC	TCGTCACACC	7560
GACAGCTTAA	CTTATAACGT	CTTAGCTGCT	CGTCGAGGTG	ACGCCACTTG	CGATGCCATC	7620
CAGAAGGCTG	CGGAATTGGT	GAACAAGTTT	CGCGTTTTTC	CTACATCTTT	TGGTGGTAGT	7680
GTTATCAATC	TCAACGTGAA	GAAGGACGTG	GAAGATAACA	GTAGGTGCAA	GGCTTCGTCTG	7740
GCACCATTGA	GCGTAATCAA	CGACTTTTTG	AACGAAGTTA	ATCCCGGTAC	TGCGGTGATT	7800
GATTTTGGTG	ATTTGTCCGC	GGACTTCAGT	ACTGGGCCTT	TTGAGTGCGG	TGCCAGCGGT	7860
ATTGTGGTGC	GGGACAACAT	CTCCTCCAGC	AACATCACTG	ATCACGATAA	GCAGCGTGTT	7920
TAGCGTAGTT	CGGTCGCAGG	CGATTCCGCG	TAGAAAACCT	TCTCTACAAG	AAAATTTGTA	7980
TTCGTTTGAA	GCGCGGAATT	ATAACTTCTC	GACTTGCGAC	CGTAACACAT	CTGCTTCAAT	8040
GTTCGGAGAG	GCTATGGCGA	TGAACTGTCT	TCGTCGTTGC	TTCGACCTAG	ATGCCTTTTC	8100
GTCCCTGCGT	GATGATGTGA	TTAGTATCAC	ACGTTCAGGC	ATCGAACAAT	GGCTGGAGAA	8160
ACGTACTCCT	AGTCAGATTA	AAGCATTAAT	GAAGGATGTT	GAATCGCCTT	TGGAAATTGA	8220
CGATGAAATT	TGTCGTTTTA	AGTTGATGGT	GAAGCGTGAC	GCTAAGGTGA	AGTTAGACTC	8280
TTCTTGTTTA	ACTAAACACA	GCGCCGCTCA	AAATATCATG	TTTCATCGCA	AGAGCATTA	8340
TGCTATCTTC	TCTCCTATCT	TTAATGAGGT	GAAAAACCGA	ATAATGTGCT	GTCTTAAGCC	8400
TAACATAAAG	TTTTTTACGG	AGATGACTAA	CAGGGATTTT	GCTTCTGTTG	TCAGCAACAT	8460
GCTTGGTGAC	GACGATGTGT	ACCATATAGG	TGAAGTTGAT	TTCTCAAAGT	ACGACAAGTC	8520
TCAAGATGCT	TTCGTGAAGG	CTTTTGAAGA	AGTAATGTAT	AAGGAACTCG	GTGTTGATGA	8580
AGAGTTGCTG	GCTATCTGGA	TGTGCGGCGA	GCGGTTATCG	ATAGCTAACA	CTCTCGATGG	8640
TCAGTTGTCC	TTCACGATCG	AGAATCAAAG	GAAGTCGGGA	GCTTCGAACA	CTTGGATTGG	8700
TAACCTCTCTC	GTCACTTTGG	GTATTTTAAAG	TCTTTACTAC	GACGTTAGAA	ATTTCGAGGC	8760
GTTGTACATC	TCGGGCGATG	ATTCTTTAAT	TTTTTCTCGC	AGCGAGATTT	CGAATTATGC	8820
CGACGACATA	TGCACTGACA	TGGGTTTTGA	GACAAAATTT	ATGTCCCCAA	GTGTCCCGTA	8880
CTTTTGTCT	AAATTTGTTG	TTATGTGTGG	TCATAAGACG	TTTTTTGTTC	CCGACCCGTA	8940
CAAGCTTTTT	GTCAAGTTGG	GAGCAGTCAA	AGAGGATGTT	TCAATGGATT	TCCTTTTCGA	9000

GACTTTTACC TCCTTTAAAG ACTTAACCTC CGATTTTAAC GACGAGCGCT TAATTCAAAA	9060
GCTCGCTGAA CTTGTGGCTT TAAAATATGA GGTTCAAACC GGCAACACCA CCTTGGCGTT	9120
AAGTGTGATA CATTGTTTGC GTTCGAATTT CCTCTCGTTT AGCAAGTTAT ATCCTCGCGT	9180
GAAGGGATGG CAGGTTTTTT ACACGTCGGT TAAGAAAGCG CTTCTCAAGA GTGGGTGTTC	9240
TCTCTTCGAC AGTTTCATGA CCCCTTTTGG TCAGGCTGTC ATGGTTTGGG ATGATGAGTA	9300
GCGCTAACTT GTGCGCAGTT TCTTTGTTCG TGACATACAC CTTGTGTGTC ACCGTGCGTT	9360
TATAATGAAT CAGGTTTTGC AGTTTGAATG TTTGTTTCTG CTGAATCTCG CGGTTTTTGC	9420
TGTGACTTTC ATTTTCATTC TTCTGGTCTT CCGCGTGATT AAGTCTTTTC GCCAGAAGGG	9480
TCACGAAGCA CCTGTTCCCG TTGTTCGTGG CGGGGGTTTT TCAACCGTAG TGTAGTCAAA	9540
AGACGCGCAT ATGGTAGTTT TCGGTTTGGG CTTTGGCACC ACATTCTCTA CGGTGTGTGT	9600
GTACAAGGAT GGACGAGTTT TTTCATTCAA GCAGAATAAT TCGGCGTACA TCCCCACTTA	9660
CCTCTATCTC TTCTCCGATT CTAACCACAT GACTTTTGGT TACGAGGCCG AATCACTGAT	9720
GAGTAATCTG AAAGTTAAAG GTTCGTTTTA TAGAGATTTA AAACGTTGGG TGGGTGCGA	9780
TTGAGTAAC CTCGACGCGT ACCTTGACCG TTTAAACCT CATTACTCGG TCCGCTTGGT	9840
TAAGATCGGC TCTGGCTTGA ACGAACTGT TTCAATTGGA AACTTCGGGG GCACTGTAA	9900
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GGAGGGCGCG TTTGCGTGCA CTTGCACCGG GGTATTTGT TCAGTACCTG CCAATTATGA	10020
TAGCGTTCAA AGGAATTTCA CTGATCAGTG TGTTTCACTC AGCGGTTATC AGTGCGTATA	10080
TATGATCAAT GAACCTTCAG CGGCTGCGCT ATCTGCGTGT AATTCGATTG GAAAGAAGTC	10140
CGCAAATTTG GCTGTTTACG ATTTGCGTGG TGGGACCTTC GACGTGTCTA TCATTTCATA	10200
CCGCAACAAT ACTTTTGTTG TGCGAGCTTC TGGAGGCGAT CTAAATCTCG GTGGAAGGGA	10260
TGTTGATCGT GCGTTTCTCA CGCACCTCTT CTCTTTAACA TCGCTGGAAC CTGACCTCAC	10320
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TTTGAGAGGT GTCGATGGAA GAAAAGAAGA CGTTAGAGTA AACAAAAACA TTCTTACGTC	10440
GGTGATGCTC CCCTACGTGA ACAGAACGCT TAAGATATTA GAGTCAACCT TAAAATCGTA	10500
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TTCATATCTT CCTGGCCTGG CAGACGTAAC AACGAAGCAT CAGAGCGTTG ATCGTATCTT	10620
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CTCAGGATCT GGGGGGTTGC TACTGATCGA CTGTGCAGCT CACACTGTCTG CTATAGCGGA	10740
CAGAAGTTGT CATCAAATCA TTTGCGCTCC AGCGGGGGCA CCGATCCCCT TTTCAGGAAG	10800
CATGCCTTTG TACTTAGCCA GGGTCAACAA GAACTCGCAG CGTGAAGTCG CCGTGTGTTGA	10860

AGGGGAGTAC	GTTAAGTGCC	CTAAGAACAG	AAAGATCTGT	GGAGCAAATA	TAAGATTTTT	10920	
TGATATAGGA	GTGACGGGTG	ATTCGTACGC	ACCCGTTACC	TTCTATATGG	ATTTCTCCAT	10980	
TTCAAGCGTA	GGAGCCGTTT	CATTCGTGGT	GAGAGGTCCT	GAGGGTAAGC	AAGTGTCACT	11040	
CACTGGAAC	CCAGCGTATA	ACTTTTCGTC	TGTGGCTCTC	GGATCACGCA	GTGTCCGAGA	11100	
ATTGCATATT	AGTTTAAATA	ATAAAGTTTT	TCTCGGTTTG	CTTCTACATA	GAAAGGCGGA	11160	
TCGACGAATA	CTTTTCACTA	AGGATGAAGC	GATTCGATAC	GCCGATTCAA	TTGATATCGC	11220	
GGATGTGCTA	AAGGAATATA	AAAGTTACGC	GGCCAGTGCC	TTACCACCAG	ACGAGGATGT	11280	
CGAATTACTC	CTGGGAAAGT	CTGTTCAAAA	AGTTTACGG	GGAAGCAGAC	TGGAAGAAAT	11340	
ACCTCTCTAG	GAGCATAGCA	GCACACTCAA	GTGAAATTAA	AACTCTACCA	GACATTCGAT	11400	
TGTACGGCGG	TAGGGTTGTA	AAGAAGTCCG	AATTCGAATC	AGCACTTCCT	AATTCTTTTG	11460	
AACAGGAATT	AGGACTGTTC	ATACTGAGCG	AACGGGAAGT	GGGATGGAGC	AAATTATGCG	11520	
GAATAACGGT	GGAAGAAGCA	GCATACGATC	TTACGAATCC	CAAGGCTTAT	AAATTCACTG	11580	
CCGAGACATG	TAGCCCGGAT	GTAAAAGGTG	AAGGACAAAA	ATACTCTATG	GAAGACGTGA	11640	
TGAATTTTCA	TGCGTTTATCA	AATCTGGATG	TTAACGACAA	GATGCTGACG	GAACAGTGTT	11700	
GGTCGCTGTC	CAATTCATGC	GGTGAATTGA	TCAACCCAGA	CGACAAAGGG	CGATTCGTGG	11760	
CTCTCACCTT	TAAGGACAGA	GACACAGCTG	ATGACACGGG	TGCCGCCAAC	GTGGAATGTC	11820	
GCGTGGGCGA	CTATCTAGTT	TACGCTATGT	CCCTGTTTGA	GCAGAGGACC	CAAAAATCGC	11880	
AGTCTGGCAA	CATCTCTCTG	TACGAAAAGT	ACTGTGAATA	CATCAGGACC	TACTTAGGGA	11940	
GTACAGACCT	GTTCTTCACA	GCGCCGGACA	GGATTCCGTT	ACTTACGGGC	ATCCTATACG	12000	
ATTTTTGTAA	GGAATACAAC	GTTTTCTACT	CGTCATATAA	GAGAAACGTC	GATAATTTCA	12060	
GATTCTTCTT	GGCGAATTAT	ATGCCTTTGA	TATCTGACGT	CTTTGTCTTC	CAGTGGGTAA	12120	
AACCCGCGCC	GGATGTTTCG	CTGCTTTTTG	AGTTAAGTGC	AGCGGAAC	ACGCTGGAGG	12180	
TTCCACACT	GAGTTTGATA	GATTCTCAAG	TTGTGGTAGG	TCATATCTTA	AGATACGTAG	12240	
AATCCTACAC	ATCAGATCCA	GCCATCGACG	CGTTAGAAGA	CAAAC	TGGAA	GCGATACTGA	12300
AAAGTAGCAA	TCCCCGTCTA	TCGACAGCGC	AACTATGGGT	TGGTTTCTTT	TGTTACTATG	12360	
GTGAGTTTCG	TACGGCTCAA	AGTAGAGTAG	TGCAAAGACC	AGGCGTATAC	AAAACACCTG	12420	
ACTCAGTGGG	TGGATTTGAA	ATAAACATGA	AAGATGTTGA	GAAATTCTTC	GATAAACTTC	12480	
AGAGAGAATT	GCCTAATGTA	TCTTTGCGGC	GTCAGTTTAA	CGGAGCTAGA	GCGCATGAGG	12540	
CTTTCAAAAT	ATTTAAAAAC	GGAAATATAA	GTTTCAGACC	TATATCGCGT	TTAAACGTGC	12600	
CTAGAGAGTT	CTGGTATCTG	AACATAGACT	ACTTCAGGCA	CGCGAATAGG	TCCGGGTAA	12660	

CCGAAGAAGA	AATACTCATC	CTAAACAACA	TAAGCGTTGA	TGTTAGGAAG	TTATGCGCTG	12720
AGAGAGCGTG	CAATACCCTA	CCTAGCGCGA	AGCGCTTTAG	TAAAAATCAT	AAGAGTAATA	12780
TACAATCATC	ACGCCAAGAG	CGGAGGATTA	AAGACCCATT	GGTAGTCCTG	AAAGACACTT	12840
TATATGAGTT	CCAACACAAG	CGTGCCGGTT	GGGGGTCTCG	AAGCACTCGA	GACCTCGGGA	12900
GTCGTGCTGA	CCACGCGAAA	GGAAGCGGTT	GATAAGTTTT	TTAATGAACT	AAAAAACGAA	12960
AATTACTCAT	CAGTTGACAG	CAGCCGATTA	AGCGATTTCGG	AAGTAAAAGA	AGTGTTAGAG	13020
AAAAGTAAAG	AAAGTTTCAA	AAGCGAACTG	GCCTCCACTG	ACGAGCACTT	CGTCTACCAC	13080
ATTATATTTT	TCTTAATCCG	ATGTGCTAAG	ATATCGACAA	GTGAAAAGGT	GAAGTACGTT	13140
GGTAGTCATA	CGTACGTGGT	CGACGGAAAA	ACGTACACCG	TTCTTGACGC	TTGGGTATTC	13200
AACATGATGA	AAAGTCTCAC	GAAGAAGTAC	AAACGAGTGA	ATGGTCTGCG	TGCGTTCTGT	13260
TGCGCGTGCG	AAGATCTATA	TCTAACCGTC	GCACCAATAA	TGTCAGAACG	CTTTAAGACT	13320
AAAGCCGTAG	GGATGAAAGG	TTTGCCTGTT	GGAAAGGAAT	ACTTAGGCGC	CGACTTTCTT	13380
TCGGGAACTA	GCAAACGTAT	GAGCGATCAC	GACAGGGCGG	TCTCCATCGT	TGCAGCGAAA	13440
AACGCTGTCT	ATCGTAGCGC	TTTCACGGGT	GGGGAGAGAA	AGATAGTTAG	TTTGTATGAT	13500
CTAGGGAGGT	ACTAAGCACG	GTGTGCTATA	GTGCGTGCTA	TAATAATAAA	CACTAGTGCT	13560
TAAGTCGCGC	AGAAGAAAAC	GCTATGGAGT	TGATGTCCGA	CAGCAACCTT	AGCAACCTGG	13620
TGATAACCGA	CGCCTCTAGT	CTAAATGGTG	TCGACAAGAA	GCTTTTATCT	GCTGAAGTTG	13680
AAAAAATGTT	GGTGCAGAAA	GGGGCTCCTA	ACGAGGGTAT	AGAAGTGGTG	TTCGGTCTAC	13740
TCCTTTACGC	ACTCGCGGCA	AGAACCACGT	CTCCTAAGGT	TCAGCGCGCA	GATTCAGACG	13800
TTATATTTTC	AAATAGTTTC	GGAGAGAGGA	ATGTGGTAGT	AACAGAGGGT	GACCTTAAGA	13860
AGGTACTCGA	CGGGTGTGCG	CCTCTCACTA	GGTTCACTAA	TAACTTAGA	ACGTTCCGTC	13920
GTACTTTTAC	TGAGGCTTAC	GTTGACTTTT	GTATCGCGTA	TAAGCACAAA	TTACCCCAAC	13980
TCAACGCCGC	GGCGGAATTG	GGGATTCCAG	CTGAAGATTC	GTACTTAGCT	GCAGATTTTC	14040
TGGGTACTTG	CCCGAAGCTC	TCTGAATTAC	AGCAAAGTAG	GAAGATGTTT	GCGAGTATGT	14100
ACGCTCTAAA	AACTGAAGGT	GGAGTGGTAA	ATACACCAGT	GAGCAATCTG	CGTCAGCTAG	14160
GTAGAAGGGA	AGTTATGTAA	TGGAAGATTA	CGAAGAAAAA	TCCGAATCGC	TCATACTGCT	14220
ACGCACGAAT	CTGAACACTA	TGCTTTTAGT	GGTCAAGTCC	GATGCTAGTG	TAGAGCTGCC	14280
TAAACTACTA	ATTTGCGGTT	ACTTACGAGT	GTCAGGACGT	GGGGAGGTGA	CGTGTGTCAG	14340
CCGTGAGGAA	TTAACAAGAG	ATTTTGAGGG	CAATCATCAT	ACGGTGATCC	GTTCTAGAAT	14400
CATACAATAT	GACAGCGAGT	CTGCTTTTGA	GGAATTCAAC	AACTCTGATT	GCGTAGTGAA	14460
GTTTTTCCTA	GAGACTGGTA	GTGTCTTTTG	GTTTTTCCTT	CGAAGTGAAA	CCAAAGGTAG	14520

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AGCGGTGCGA CATTTCGCGA CCTTCTTCGA AGCTAACAAAT TTCTTCTTTG GATCGCATTG 14580
CGGTACCATG GAGTATTGTT TGAAGCAGGT ACTAACTGAA ACTGAATCTA TAATCGATTG 14640
TTTTTGCGAA GAAAGAAATC GTTAAGATGA GGGTTATAGT GTCTCCTTAT GAAGCTGAAG 14700
ACATTCTGAA AAGATCGACT GACATGTTAC GAAACATAGA CAGTGGGGTC TTGAGCACTA 14760
AAGAATGTAT CAAGGCATTC TCGACGATAA CGCGAGACCT ACATTGTGCG AAGGCTTCCT 14820
ACCAGTGGGG TGTTGACACT GGGTTATATC AGCGTAATTG CGCTGAAAAA CGTTTAATTG 14880
ACACGGTGGA GTCAAACATA CGGTTGGCTC AACCTCTCGT GCGTGAAAAA GTGGCGGTTC 14940
ATTTTTGTAA GGATGAACCA AAAGAGCTAG TAGCATTTCAT CACGCGAAAG TACGTGGAAC 15000
TCACGGGCGT GGGAGTGAGA GAAGCGGTGA AGAGGGAAAT GCGCTCTCTT ACCAAAACAG 15060
TTTTAAATAA AATGTCTTTG GAAATGGCGT TTTACATGTC ACCACGAGCG TGGAAAAACG 15120
CTGAATGGTT AGAACTAAAA TTTTCACCTG TGAAAATCTT TAGAGATCTG CTATTAGACG 15180
TGGAAACGCT CAACGAATTG TGCGCCGAAG ATGATGTTCA CGTCGACAAA GTAAATGAGA 15240
ATGGGGACGA AAATCACGAC CTCGAACTCC AAGACGAATG TTAAACATTG GTTAAGTTTA 15300
ACGAAAATGA TTAGTAAATA ATAAATCGAA CGTGGGTGTA TCTACCTGAC GTATCAACTT 15360
AAGCTGTTAC TGAGTAATTA AACCAACAAG TGTGGGTGTA ATGTGTATGT TGATGTAGAG 15420
AAAAATCCGT TTGTAGAACG GTGTTTTTCT CTTCTTTATT TTTAAAAAAA AAATAAAAAA 15480
AAAAAAAAAA AAGCGGCCGC 15500

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Another DNA molecule of the present invention (GLRaV-2 ORF1a) includes nucleotides 4-7923 of SEQ. ID. No. 1 and is believed to code for a large, grapevine leafroll virus polyprotein containing the conserved domains characteristic of two papain-like proteases, a methyltransferase, and a helicase. This DNA molecule comprises the nucleotide

5 sequence corresponding to SEQ. ID. No. 2 as follows:

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ACATTGCGAG AGAACCCCAT TAGCGTCTCC GGGGTGAACT TGGGAAGGTC TGCCGCCGCT 60
CAGGTTATTT ATTTTCGGCAG TTTCACGCAG CCCTTCGCGT TGTATCCGCG CCAAGAGAGC 120
GCGATCGTAA AAACGCAACT TCCACCGGTC AGTGTAGTGA AGGTGGAGTG CGTAGCTGCG 180
GAGGTAGCTC CCGACAGGGG CGTGGTCGAC AAGAAACCTA CGTCTGTTGG CGTTCCCCCG 240
CAGCGCGGTG TGCTTTCTTT TCCGACGGTG GTTCGGAACC GCGGCGACGT GATAATCACA 300
GGGGTGGTGC ATGAAGCCCT GAAGAAAATT AAAGACGGGC TCTTACGCTT CCGCGTAGGC 360
GGTGACATGC GTTTTTTCGAG ATTTTCTCA TCGAACTACG GCTGCAGATT CGTCGCGAGC 420
GTGCGTACGA AACTACAGT TTGGCTAAAT TGCACGAAAG CGAGTGGTGA GAAATTCTCA 480

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CTCGCCGCCG CGTGCACGGC GGATTACGTG GCGATGCTGC GTTATGTGTG TGGCGGGAAA	540
TTTCCACTCG TCCTCATGAG TAGAGTTATT TACCCGGATG GGCGCTGTTA CTTGGCCCAT	600
ATGAGGTATT TGTGCGCCTT TTACTGTGCG CCGTTTAGAG AGTCGGATTA TGCCCTCGGA	660
ATGTGGCCTA CGGTGGCGCG TCTCAGGGCA TGCGTTGAGA AGAACTTCGG TGTCGAAGCT	720
TGTGGCATAG CTCTTCGTGG CTATTACACC TCTCGCAATG TTTATCACTG TGATTATGAC	780
TCTGCTTATG TAAAATATTT TAGAAACCTT TCCGGCCGCA TTGGCGGTGG TTCGTTCGAT	840
CCGACATCTT TAACCTCCGT AATAACGGTG AAGATTAGCG GTCTTCCAGG TGGTCTTCCT	900
AAAAATATAG CGTTTGGTGC CTTCTGTGCG GATATACGTT ACGTCGAACC GGTAGACTCG	960
GGCGGCATTC AATCGAGCGT TAAGACGAAA CGTGAAGATG CGCACCGAAC CGTAGAGGAA	1020
CGGGCGGCCG GCGGATCCGT CGAGCAACCG CGACAAAAGA GGATAGATGA GAAAGGTTGC	1080
GGCAGAGTTC CTAGTGGAGG TTTTTCGCAT CTCCTGGTCG GCAACCTTAA CGAAGTTAGG	1140
AGGAAGGTAG CTGCCGGACT TCTACGCTTT CGCGTTGGCG GTGATATGGA TTTTCATCGC	1200
TCGTTCTCCA CCCAAGCGGG CCACCGCTTG CTGGTGTGGC GCCGCTCGAG CCGGAGCGTG	1260
TGCCTTGAAC TTTACTCACC ATCTAAAAAC TTTTTCGCTT ACGATGTCTT GCCCTGTTCT	1320
GGAGACTATG CAGCGATGTT TTCTTTCGCG GCGGGCGGCC GTTTCCTTTT AGTTTTGATG	1380
ACTAGAATTA GATACCCGAA CGGGTTTTGT TACTTGGCTC ACTGCCGGTA CGCGTGC GCG	1440
TTTCTCTTAA GGGGTTTTGA TCCGAAGCGT TTCGACATCG GTGCTTTCCC CACCGCGGCC	1500
AAGCTCAGAA ACCGTATGGT TTCGGAGCTT GGTGAAAGAA GTTTAGGTTT GAACTTGTAC	1560
GGCGCATATA CGTCACGCGG CGTCTTTCAC TGCGATTATG ACGCTAAGTT TATAAAGGAT	1620
TTGCGTCTTA TGTCAGCAGT TATAGCTGGA AAGGACGGGG TGGAAGAGGT GGTACCTTCT	1680
GACATAACTC CTGCCATGAA GCAGAAAACG ATCGAAGCCG TGTATGATAG ATTATATGGC	1740
GGCACTGACT CGTTGCTGAA ACTGAGCATC GAGAAAGACT TAATCGATTT CAAAAATGAC	1800
GTGCAGAGTT TGAAGAAAGA TCGGCCGATT GTCAAAGTGC CCTTTTACAT GTCGGAAGCA	1860
ACACAGAATT CGCTGACGCG TTTCTACCCT CAGTTCGAAC TTAAGTTTTC GCACTCCTCG	1920
CATTCAGATC ATCCCGCCGC CGCCGCTTCT AGACTGCTGG AAAATGAAAC GTTAGTGCGC	1980
TTATGTGGTA ATAGCGTTTC AGATATTGGA GGTGTCTCTC TTTTCCATTT GCATTCCAAG	2040
ACGCAAAGAC GGGTTCACGT ATGTAGGCCT GTGTTGGATG GCAAGGATGC GCAGCGTCGC	2100
GTGGTGCGTG ATTTGCAGTA TTCCAACGTG CGTTTGGGAG ACGATGATAA AATTTTGGAA	2160
GGGCCACGCA ATATCGACAT TTGCCACTAT CCTCTGGGCG CGTGTGACCA CGAAAGTAGT	2220
GCTATGATGA TGGTGCAGGT GTATGACGCG TCCCTTTATG AGATATGTGG CGCCATGATC	2280

AAGAAGAAAA	GCCGCATAAC	GTA CTTAACC	ATGGTCACGC	CCGGCGAGTT	TCTTGACGGA	2340
CGCGAATGCG	TCTACATGGA	GTCGTTAGAC	TGTGAGATTG	AAGTTGATGT	GCACGCGGAC	2400
GTCGTAATGT	ACAAATTCGG	TAGTTCTTGC	TATTCGCACA	AGCTTTCAAT	CATCAAGGAC	2460
ATCATGACCA	CTCCGTACTT	GACACTAGGT	GGTTTTCTAT	TCAGCGTGGA	GATGTATGAG	2520
GTGCGTATGG	GCGTGAATTA	CTTCAAGATT	ACGAAGTCCG	AAGTATCGCC	TAGCATTAGC	2580
TGCACCAAGC	TCCTGAGATA	CCGAAGAGCT	AATAGTGACG	TGGTTAAAGT	TAAACTTCCA	2640
CGTTTCGATA	AGAAACGTCG	CATGTGTCTG	CCTGGGTATG	ACACCATATA	CCTAGATTCTG	2700
AAGTTTGTGA	GTCGCGTTTT	CGATTATGTC	GTGTGTAATT	GCTCTGCCGT	GAACTCAAAA	2760
ACTTTCGAGT	GGGTGTGGAG	TTTCATTAAG	TCTAGTAAGT	CGAGGGTGAT	TATTAGCGGT	2820
AAAATAATTC	ACAAGGATGT	GAATTTGGAC	CTCAAGTACG	TCGAGAGTTT	CGCCGCGGTT	2880
ATGTTGGCCT	CTGGCGTGCG	CAGTAGACTA	GCGTCCGAGT	ACCTTGCTAA	GAACCTTAGT	2940
CATTTTTTCGG	GAGATTGCTC	CTTTATTGAA	GCCACGTCTT	TCGTGTTGCG	TGAGAAAATC	3000
AGAAACATGA	CTCTGAATTT	TAACGAAAGA	CTTTTACAGT	TAGTGAAGCG	CGTTGCCTTT	3060
GCGACCTTGG	ACGTGAGTTT	TCTAGATTTA	GATTCAACTC	TTGAATCAAT	AACTGATTTT	3120
GCCGAGTGTA	AGGTAGCGAT	TGAACTCGAC	GAGTTGGGTT	GCTTGAGAGC	GGAGGCCGAG	3180
AATGAAAAAA	TCAGGAATCT	GGCGGGAGAT	TCGATTGCGG	CTAAACTCGC	GAGCGAGATA	3240
GTGGTCGATA	TTGACTCTAA	GCCTTCACCG	AAGCAGGTGG	GTAATTCGTC	ATCCGAAAAC	3300
GCCGATAAGC	GGGAAGTTCA	GAGGCCCGGT	TTGCGTGGTG	GTTCTAGAAA	CGGGGTTGTT	3360
GGGGAGTTCC	TTCACTTCGT	CGTGGATTCT	GCCTTGCGTC	TTTTCAAATA	CGCGACGGAT	3420
CAACAACGGA	TCAAGTCTTA	CGTGCGTTTC	TTGGACTCGG	CGGTCTCATT	CTTGGATTAC	3480
AACTACGATA	ATCTATCGTT	TATACTGCGA	GTGCTTTCGG	AAGGTTATTC	GTGTATGTTC	3540
GCGTTTTTGG	CGAATCGCGG	CGACTTATCT	AGTCGTGTCC	GTAGCGCGGT	GTGTGCTGTG	3600
AAAGAAGTTG	CTACCTCATG	CGCGAACGCG	AGCGTTTCTA	AAGCCAAGGT	TATGATTACC	3660
TTCGCAGCGG	CCGTGTGTGC	TATGATGTTT	AATAGCTGCG	GTTTTTCAGG	CGACGGTCGG	3720
GAGTATAAAT	CGTATATACA	TCGTTACACG	CAAGTATTGT	TTGACACTAT	CTTTTTTGAG	3780
GACAGCAGTT	ACCTACCCAT	AGAAGTTCTG	AGTTCGGCGA	TATGCGGTGC	TATCGTCACA	3840
CTTTTCTCCT	CGGGCTCGTC	CATAAGTTTA	AACGCCTTCT	TACTTCAAAT	TACCAAAGGA	3900
TTCTCCCTAG	AGGTTGTCTG	CCGGAATGTT	GTGCGAGTCA	CGCATGGTTT	GAGCACCACA	3960
GCGACCGACG	GCGTCATACG	TGGGGTTTTT	TCCCAAATTG	TGTCTCACTT	ACTTGTTGGA	4020
AATACGGGTA	ATGTGGCTTA	CCAGTCAGCT	TTCATTGCCG	GGGTGGTGCC	TCTTTTAGTT	4080
AAAAAGTGTG	TGAGCTTAAT	CTTCATCTTG	CGTGAAGATA	CTTATTCCGG	TTTTATTAAG	4140

CACGGAATCA	GTGAATTCTC	TTTCCTTAGT	AGTATTCTGA	AGTTCTTGAA	GGGTAAGCTT	4200
GTGGACGAGT	TGAAATCGAT	TATTCAAGGG	GTTTTTGATT	CCAACAAGCA	CGTGTTTAAA	4260
GAAGCTACTC	AGGAAGCGAT	TCGTACGACG	GTCATGCAAG	TGCCTGTCGC	TGTAGTGGAT	4320
GCCCTTAAGA	GCGCCGCGGG	AAAAATTTAT	AACAATTTTA	CTAGTCGACG	TACCTTTGGT	4380
AAGGATGAAG	GCTCCTCTAG	CGACGGCGCA	TGTGAAGAGT	ATTTCTCATG	CGACGAAGGT	4440
GAAGGTCCGG	GTCTGAAAGG	GGGTTCCAGC	TATGGCTTCT	CAATTTTAGC	GTTCTTTTCA	4500
CGCATTATGT	GGGGAGCTCG	TCGGCTTATT	GTTAAGGTGA	AGCATGAGTG	TTTTGGGAAA	4560
CTTTTTGAAT	TTCTATCGCT	CAAGCTTCAC	GAATTCAGGA	CTCGCGTTTT	TGGGAAGAAT	4620
AGAACGGACG	TGGGAGTTTA	CGATTTTTTG	CCCACGGGCA	TCGTGGAAAC	GCTCTCATCG	4680
ATAGAAGAGT	GCGACCAAAT	TGAAGAACTT	CTCGGCGACG	ACCTGAAAGG	TGACAAGGAT	4740
GCTTCGTTGA	CCGATATGAA	TTACTTTGAG	TTCTCAGAAG	ACTTCTTAGC	CTCTATCGAG	4800
GAGCCGCCTT	TCGCTGGATT	GCGAGGAGGT	AGCAAGAACA	TCGCGATTTT	GGCGATTTTG	4860
GAATACGCGC	ATAATTTGTT	TCGCATTGTC	GCAAGCAAGT	GTTGAAACG	ACCTTTATTT	4920
CTTGCTTTTCG	CCGAACCTCTC	AAGCGCCCTT	ATCGAGAAAT	TTAAGGAGGT	TTTCCCTCGT	4980
AAGAGCCAGC	TCGTCGCTAT	CGTGCGCGAG	TATACTCAGA	GATTCCCTCCG	AAGTCGCATG	5040
CGTGCGTTGG	GTTTGAATAA	CGAGTTCGTG	GTAAAATCTT	TCGCCGATTT	GCTACCCGCA	5100
TTAATGAAGC	GGAAGGTTTC	AGGTTCGTTC	TTAGCTAGTG	TTTATCGCCC	ACTTAGAGGT	5160
TTCTCATATA	TGTGTGTTTC	AGCGGAGCGA	CGTGAAAAGT	TTTTTGCTCT	CGTGTGTTTA	5220
ATCGGGTTAA	GTCTCCCTTT	CTTCGTGCGC	ATCGTAGGAG	CGAAAGCGTG	CGAAGAACTC	5280
GTGTCCTCAG	CGCGTCGCTT	TTATGAGCGT	ATTAAATTTT	TTCTAAGGCA	GAAGTATGTC	5340
TCTCTTTCTA	ATTTCTTTTG	TCACTTGTTT	AGCTCTGACG	TTGATGACAG	TTCCGCATCT	5400
GCAGGGTTGA	AAGGTGGTGC	GTCGCGAATG	ACGCTCTTCC	ACCTTCTGGT	TCGCCTTGCT	5460
AGTGCCCTCC	TATCGTTAGG	GTGGGAAGGG	TTAAAGCTAC	TCTTATCGCA	CCACAATTG	5520
TTATTTTTGT	GTTTTGCATT	GGTTGACGAT	GTGAACGTCC	TTATCAAAGT	TCTTGGGGGT	5580
CTTTCTTTCT	TTGTGCAACC	AATCTTTTCC	TTGTTTGCGG	CGATGCTTCT	ACAACCGGAC	5640
AGGTTTGTGG	AGTATTCCGA	GAAACTTGTT	ACAGCGTTTG	AATTTTCTT	AAAATGTTTCG	5700
CCTCGCGCGC	CTGCACTACT	CAAAGGGTTT	TTTGAGTGCG	TGGCGAACAG	CACTGTGTCA	5760
AAAACCGTTC	GAAGACTTCT	TCGCTGTTTC	GTGAAGATGC	TCAAACCTCG	AAAAGGGCGA	5820
GGGTTGCGTG	CGGATGGTAG	GGGTCTCCAT	CGGCAGAAAG	CCGTACCCGT	CATACCTTCT	5880
AATCGGGTCG	TGACCGACGG	GGTTGAAAGA	CTTTCGGTAA	AGATGCAAGG	AGTTGAAGCG	5940

TTGCGTACCG AATTGAGAAT CTTAGAAGAT TTAGATTCTG CCGTGATCGA AAAACTCAAT	6000
AGACGCAGAA ATCGTGACAC TAATGACGAC GAATTTACGC GCCCTGCTCA TGAGCAGATG	6060
CAAGAAGTCA CCACTTTCTG TTCGAAAGCC AACTCTGCTG GTTTGGCCCT GGAAAGGGCA	6120
GTGCTTGTGG AAGACGCTAT AAAGTCGGAG AAACTTTCTA AGACGGTTAA TGAGATGGTG	6180
AGGAAAGGGA GTACCACCAG CGAAGAAGTG GCCGTCGCTT TGTCGGACGA TGAAGCCGTG	6240
GAAGAAATCT CTGTTGCTGA CGAGCGAGAC GATTGCGCTA AGACAGTCAG GATAAGCGAA	6300
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AAGGATACCG GGGGTCTAAC GAACGCCGTG AGGGAGTTTT ATTATATGCA AGAACTTGCT	6420
CTTTTCGAAA TCCACAGCAA ACTGTGCACC TACTACGATC AACTGCGCAT AGTCAACTTC	6480
GATCGTTCCG TAGCACCATG CAGCGAAGAT GCTCAGCTGT ACGTACGGAA GAACGGCTCA	6540
ACGATAGTGC AGGGTAAAGA GGTACGTTTG CACATTAAGG ATTTCCACGA TCACGATTTT	6600
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GACAACCTCG CGTTCCTGGC GAGTAATTTG TTCTTAGCCG GCTACCCCTT TTCAAGGAGC	6720
TTCGTCTTCA CGAATTCGTC GGTGATATT CTCCTCTACG AAGCTCCACC CGGAGGTGGT	6780
AAGACGACGA CGCTGATTGA CTCGTTCTTG AAGGTCTTCA AGAAAGGTGA GGTTCACC	6840
ATGATCTTAA CCGCCAACAA AAGTTCGCAG GTTGAGATCC TAAAGAAAGT GGAGAAGGAA	6900
GTGTCTAACA TTGAATGCCA GAAACGTAAA GACAAAAGAT CTCCGAAAAA GAGCATTTAC	6960
ACCATCGACG CTTATTTAAT GCATCACCGT GGTGTGATG CAGACGTTCT TTTCATCGAT	7020
GAGTGTTTCA TGGTTCATGC GGGTAGCGTA CTAGCTTGCA TTGAGTTCAC GAGGTGTCAT	7080
AAAGTAATGA TCTTCGGGGA TAGCCGGCAG ATTCACTACA TTGAAAGGAA CGAATTGGAC	7140
AAGTGTTTGT ATGGGGATCT CGACAGGTTT GTGGACCTGC AGTGTCGGGT TTATGGTAAT	7200
ATTTTCGTACC GTTGTCATG GGATGTGTGC GCTTGTTTAA GCACAGTGTA TGGCAACCTA	7260
ATCGCCACCG TGAAGGGTGA AAGCGAAGGT AAGAGCAGCA TGCGCATTAA CGAAATTAAT	7320
TCAGTCGACG ATTTAGTCCC CGACGTGGGT TCCACGTTTC TGTGTATGCT TCAGTCGGAG	7380
AAGTTGGAAA TCAGCAAGCA CTTTATTCGC AAGGGTTTGA CTAAACTTAA CGTCTAACG	7440
GTGCATGAGG CGCAAGGTGA GACGTATGCG CGTGTGAACC TTGTGCGACT TAAGTTTCAG	7500
GAGGATGAAC CCTTTAAATC TATCAGGCAC ATAACCGTCG CTCTTTCTCG TCACACCGAC	7560
AGCTTAACTT ATAACGTCTT AGCTGCTCGT CGAGGTGACG CCACTTGCGA TGCCATCCAG	7620
AAGGCTGCGG AATTGGTGAA CAAGTTTCGC GTTTTTCTTA CATCTTTTGG TGGTAGTGTT	7680
ATCAATCTCA ACGTGAAGAA GGACGTGGAA GATAACAGTA GGTGCAAGGC TTCGTCGGCA	7740
CCATTGAGCG TAATCAACGA CTTTTTGAAC GAAGTTAATC CCGGTACTGC GGTGATTGAT	7800

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TTTGGTGATT TGTCCGCGGA CTTCAGTACT GGGCCTTTTG AGTGCGGTGC CAGCGGTATT 7860
 GTGGTGCGGG ACAACATCTC CTCCAGCAAC ATCACTGATC ACGATAAGCA GCGTGTTTAG 7920

The large polypeptide (papain-like proteases, methyltransferase, and helicase) has an amino acid sequence corresponding to SEQ. ID. No. 3 as follows:

Thr	Leu	Arg	Glu	Asn	Pro	Ile	Ser	Val	Ser	Gly	Val	Asn	Leu	Gly	Arg	1	5	10	15
Ser	Ala	Ala	Ala	Gln	Val	Ile	Tyr	Phe	Gly	Ser	Phe	Thr	Gln	Pro	Phe	20	25	30	
Ala	Leu	Tyr	Pro	Arg	Gln	Glu	Ser	Ala	Ile	Val	Lys	Thr	Gln	Leu	Pro	35	40	45	
Pro	Val	Ser	Val	Val	Lys	Val	Glu	Cys	Val	Ala	Ala	Glu	Val	Ala	Pro	50	55	60	
Asp	Arg	Gly	Val	Val	Asp	Lys	Lys	Pro	Thr	Ser	Val	Gly	Val	Pro	Pro	65	70	75	80
Gln	Arg	Gly	Val	Leu	Ser	Phe	Pro	Thr	Val	Val	Arg	Asn	Arg	Gly	Asp	85	90	95	
Val	Ile	Ile	Thr	Gly	Val	Val	His	Glu	Ala	Leu	Lys	Lys	Ile	Lys	Asp	100	105	110	
Gly	Leu	Leu	Arg	Phe	Arg	Val	Gly	Gly	Asp	Met	Arg	Phe	Ser	Arg	Phe	115	120	125	
Phe	Ser	Ser	Asn	Tyr	Gly	Cys	Arg	Phe	Val	Ala	Ser	Val	Arg	Thr	Asn	130	135	140	
Thr	Thr	Val	Trp	Leu	Asn	Cys	Thr	Lys	Ala	Ser	Gly	Glu	Lys	Phe	Ser	145	150	155	160
Leu	Ala	Ala	Ala	Cys	Thr	Ala	Asp	Tyr	Val	Ala	Met	Leu	Arg	Tyr	Val	165	170	175	
Cys	Gly	Gly	Lys	Phe	Pro	Leu	Val	Leu	Met	Ser	Arg	Val	Ile	Tyr	Pro	180	185	190	
Asp	Gly	Arg	Cys	Tyr	Leu	Ala	His	Met	Arg	Tyr	Leu	Cys	Ala	Phe	Tyr	195	200	205	
Cys	Arg	Pro	Phe	Arg	Glu	Ser	Asp	Tyr	Ala	Leu	Gly	Met	Trp	Pro	Thr	210	215	220	
Val	Ala	Arg	Leu	Arg	Ala	Cys	Val	Glu	Lys	Asn	Phe	Gly	Val	Glu	Ala	225	230	235	240
Cys	Gly	Ile	Ala	Leu	Arg	Gly	Tyr	Tyr	Thr	Ser	Arg	Asn	Val	Tyr	His	245	250	255	
Cys	Asp	Tyr	Asp	Ser	Ala	Tyr	Val	Lys	Tyr	Phe	Arg	Asn	Leu	Ser	Gly	260	265	270	

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Arg	Ile	Gly	Gly	Gly	Ser	Phe	Asp	Pro	Thr	Ser	Leu	Thr	Ser	Val	Ile		
		275					280					285					
Thr	Val	Lys	Ile	Ser	Gly	Leu	Pro	Gly	Gly	Leu	Pro	Lys	Asn	Ile	Ala		
	290					295					300						
Phe	Gly	Ala	Phe	Leu	Cys	Asp	Ile	Arg	Tyr	Val	Glu	Pro	Val	Asp	Ser		
305					310					315					320		
Gly	Gly	Ile	Gln	Ser	Ser	Val	Lys	Thr	Lys	Arg	Glu	Asp	Ala	His	Arg		
				325					330					335			
Thr	Val	Glu	Glu	Arg	Ala	Ala	Gly	Gly	Ser	Val	Glu	Gln	Pro	Arg	Gln		
		340						345					350				
Lys	Arg	Ile	Asp	Glu	Lys	Gly	Cys	Gly	Arg	Val	Pro	Ser	Gly	Gly	Phe		
		355					360					365					
Ser	His	Leu	Leu	Val	Gly	Asn	Leu	Asn	Glu	Val	Arg	Arg	Lys	Val	Ala		
	370					375					380						
Ala	Gly	Leu	Leu	Arg	Phe	Arg	Val	Gly	Gly	Asp	Met	Asp	Phe	His	Arg		
385					390					395					400		
Ser	Phe	Ser	Thr	Gln	Ala	Gly	His	Arg	Leu	Leu	Val	Trp	Arg	Arg	Ser		
				405					410					415			
Ser	Arg	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Ser	Pro	Ser	Lys	Asn	Phe	Leu		
			420					425					430				
Arg	Tyr	Asp	Val	Leu	Pro	Cys	Ser	Gly	Asp	Tyr	Ala	Ala	Met	Phe	Ser		
		435					440					445					
Phe	Ala	Ala	Gly	Gly	Arg	Phe	Pro	Leu	Val	Leu	Met	Thr	Arg	Ile	Arg		
	450					455					460						
Tyr	Pro	Asn	Gly	Phe	Cys	Tyr	Leu	Ala	His	Cys	Arg	Tyr	Ala	Cys	Ala		
465					470					475					480		
Phe	Leu	Leu	Arg	Gly	Phe	Asp	Pro	Lys	Arg	Phe	Asp	Ile	Gly	Ala	Phe		
				485					490					495			
Pro	Thr	Ala	Ala	Lys	Leu	Arg	Asn	Arg	Met	Val	Ser	Glu	Leu	Gly	Glu		
			500					505					510				
Arg	Ser	Leu	Gly	Leu	Asn	Leu	Tyr	Gly	Ala	Tyr	Thr	Ser	Arg	Gly	Val		
		515					520					525					
Phe	His	Cys	Asp	Tyr	Asp	Ala	Lys	Phe	Ile	Lys	Asp	Leu	Arg	Leu	Met		
	530					535					540						
Ser	Ala	Val	Ile	Ala	Gly	Lys	Asp	Gly	Val	Glu	Glu	Val	Val	Pro	Ser		
545					550					555				560			
Asp	Ile	Thr	Pro	Ala	Met	Lys	Gln	Lys	Thr	Ile	Glu	Ala	Val	Tyr	Asp		
				565					570					575			
Arg	Leu	Tyr	Gly	Gly	Thr	Asp	Ser	Leu	Leu	Lys	Leu	Ser	Ile	Glu	Lys		
			580					585					590				

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Asp Leu Ile Asp Phe Lys Asn Asp Val Gln Ser Leu Lys Lys Asp Arg
 595 600 605
 Pro Ile Val Lys Val Pro Phe Tyr Met Ser Glu Ala Thr Gln Asn Ser
 610 615 620
 Leu Thr Arg Phe Tyr Pro Gln Phe Glu Leu Lys Phe Ser His Ser Ser
 625 630 635 640
 His Ser Asp His Pro Ala Ala Ala Ala Ser Arg Leu Leu Glu Asn Glu
 645 650 655
 Thr Leu Val Arg Leu Cys Gly Asn Ser Val Ser Asp Ile Gly Gly Cys
 660 665 670
 Pro Leu Phe His Leu His Ser Lys Thr Gln Arg Arg Val His Val Cys
 675 680 685
 Arg Pro Val Leu Asp Gly Lys Asp Ala Gln Arg Arg Val Val Arg Asp
 690 695 700
 Leu Gln Tyr Ser Asn Val Arg Leu Gly Asp Asp Asp Lys Ile Leu Glu
 705 710 715 720
 Gly Pro Arg Asn Ile Asp Ile Cys His Tyr Pro Leu Gly Ala Cys Asp
 725 730 735
 His Glu Ser Ser Ala Met Met Met Val Gln Val Tyr Asp Ala Ser Leu
 740 745 750
 Tyr Glu Ile Cys Gly Ala Met Ile Lys Lys Lys Ser Arg Ile Thr Tyr
 755 760 765
 Leu Thr Met Val Thr Pro Gly Glu Phe Leu Asp Gly Arg Glu Cys Val
 770 775 780
 Tyr Met Glu Ser Leu Asp Cys Glu Ile Glu Val Asp Val His Ala Asp
 785 790 795 800
 Val Val Met Tyr Lys Phe Gly Ser Ser Cys Tyr Ser His Lys Leu Ser
 805 810 815
 Ile Ile Lys Asp Ile Met Thr Thr Pro Tyr Leu Thr Leu Gly Gly Phe
 820 825 830
 Leu Phe Ser Val Glu Met Tyr Glu Val Arg Met Gly Val Asn Tyr Phe
 835 840 845
 Lys Ile Thr Lys Ser Glu Val Ser Pro Ser Ile Ser Cys Thr Lys Leu
 850 855 860
 Leu Arg Tyr Arg Arg Ala Asn Ser Asp Val Val Lys Val Lys Leu Pro
 865 870 875 880
 Arg Phe Asp Lys Lys Arg Arg Met Cys Leu Pro Gly Tyr Asp Thr Ile
 885 890 895
 Tyr Leu Asp Ser Lys Phe Val Ser Arg Val Phe Asp Tyr Val Val Cys
 900 905 910

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Asn Cys	Ser	Ala	Val	Asn	Ser	Lys	Thr	Phe	Glu	Trp	Val	Trp	Ser	Phe	915	920	925
Ile Lys	Ser	Ser	Lys	Ser	Arg	Val	Ile	Ile	Ser	Gly	Lys	Ile	Ile	His	930	935	940
Lys Asp	Val	Asn	Leu	Asp	Leu	Lys	Tyr	Val	Glu	Ser	Phe	Ala	Ala	Val	945	950	955
Met Leu	Ala	Ser	Gly	Val	Arg	Ser	Arg	Leu	Ala	Ser	Glu	Tyr	Leu	Ala	965	970	975
Lys Asn	Leu	Ser	His	Phe	Ser	Gly	Asp	Cys	Ser	Phe	Ile	Glu	Ala	Thr	980	985	990
Ser Phe	Val	Leu	Arg	Glu	Lys	Ile	Arg	Asn	Met	Thr	Leu	Asn	Phe	Asn	995	1000	1005
Glu Arg	Leu	Leu	Gln	Leu	Val	Lys	Arg	Val	Ala	Phe	Ala	Thr	Leu	Asp	1010	1015	1020
Val Ser	Phe	Leu	Asp	Leu	Asp	Ser	Thr	Leu	Glu	Ser	Ile	Thr	Asp	Phe	1025	1030	1035
Ala Glu	Cys	Lys	Val	Ala	Ile	Glu	Leu	Asp	Glu	Leu	Gly	Cys	Leu	Arg	1045	1050	1055
Ala Glu	Ala	Glu	Asn	Glu	Lys	Ile	Arg	Asn	Leu	Ala	Gly	Asp	Ser	Ile	1060	1065	1070
Ala Ala	Lys	Leu	Ala	Ser	Glu	Ile	Val	Val	Asp	Ile	Asp	Ser	Lys	Pro	1075	1080	1085
Ser Pro	Lys	Gln	Val	Gly	Asn	Ser	Ser	Ser	Glu	Asn	Ala	Asp	Lys	Arg	1090	1095	1100
Glu Val	Gln	Arg	Pro	Gly	Leu	Arg	Gly	Gly	Ser	Arg	Asn	Gly	Val	Val	1105	1110	1115
Gly Glu	Phe	Leu	His	Phe	Val	Val	Asp	Ser	Ala	Leu	Arg	Leu	Phe	Lys	1125	1130	1135
Tyr Ala	Thr	Asp	Gln	Gln	Arg	Ile	Lys	Ser	Tyr	Val	Arg	Phe	Leu	Asp	1140	1145	1150
Ser Ala	Val	Ser	Phe	Leu	Asp	Tyr	Asn	Tyr	Asp	Asn	Leu	Ser	Phe	Ile	1155	1160	1165
Leu Arg	Val	Leu	Ser	Glu	Gly	Tyr	Ser	Cys	Met	Phe	Ala	Phe	Leu	Ala	1170	1175	1180
Asn Arg	Gly	Asp	Leu	Ser	Ser	Arg	Val	Arg	Ser	Ala	Val	Cys	Ala	Val	1185	1190	1195
Lys Glu	Val	Ala	Thr	Ser	Cys	Ala	Asn	Ala	Ser	Val	Ser	Lys	Ala	Lys	1205	1210	1215
Val Met	Ile	Thr	Phe	Ala	Ala	Ala	Val	Cys	Ala	Met	Met	Phe	Asn	Ser	1220	1225	1230

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Cys Gly Phe Ser Gly Asp Gly Arg Glu Tyr Lys Ser Tyr Ile His Arg
 1235 1240 1245
 Tyr Thr Gln Val Leu Phe Asp Thr Ile Phe Phe Glu Asp Ser Ser Tyr
 1250 1255 1260
 Leu Pro Ile Glu Val Leu Ser Ser Ala Ile Cys Gly Ala Ile Val Thr
 1265 1270 1275 1280
 Leu Phe Ser Ser Gly Ser Ser Ile Ser Leu Asn Ala Phe Leu Leu Gln
 1285 1290 1295
 Ile Thr Lys Gly Phe Ser Leu Glu Val Val Val Arg Asn Val Val Arg
 1300 1305 1310
 Val Thr His Gly Leu Ser Thr Thr Ala Thr Asp Gly Val Ile Arg Gly
 1315 1320 1325
 Val Phe Ser Gln Ile Val Ser His Leu Leu Val Gly Asn Thr Gly Asn
 1330 1335 1340
 Val Ala Tyr Gln Ser Ala Phe Ile Ala Gly Val Val Pro Leu Leu Val
 1345 1350 1355 1360
 Lys Lys Cys Val Ser Leu Ile Phe Ile Leu Arg Glu Asp Thr Tyr Ser
 1365 1370 1375
 Gly Phe Ile Lys His Gly Ile Ser Glu Phe Ser Phe Leu Ser Ser Ile
 1380 1385 1390
 Leu Lys Phe Leu Lys Gly Lys Leu Val Asp Glu Leu Lys Ser Ile Ile
 1395 1400 1405
 Gln Gly Val Phe Asp Ser Asn Lys His Val Phe Lys Glu Ala Thr Gln
 1410 1415 1420
 Glu Ala Ile Arg Thr Thr Val Met Gln Val Pro Val Ala Val Val Asp
 1425 1430 1435 1440
 Ala Leu Lys Ser Ala Ala Gly Lys Ile Tyr Asn Asn Phe Thr Ser Arg
 1445 1450 1455
 Arg Thr Phe Gly Lys Asp Glu Gly Ser Ser Ser Asp Gly Ala Cys Glu
 1460 1465 1470
 Glu Tyr Phe Ser Cys Asp Glu Gly Glu Gly Pro Gly Leu Lys Gly Gly
 1475 1480 1485
 Ser Ser Tyr Gly Phe Ser Ile Leu Ala Phe Phe Ser Arg Ile Met Trp
 1490 1495 1500
 Gly Ala Arg Arg Leu Ile Val Lys Val Lys His Glu Cys Phe Gly Lys
 1505 1510 1515 1520
 Leu Phe Glu Phe Leu Ser Leu Lys Leu His Glu Phe Arg Thr Arg Val
 1525 1530 1535
 Phe Gly Lys Asn Arg Thr Asp Val Gly Val Tyr Asp Phe Leu Pro Thr
 1540 1545 1550

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Gly Ile Val Glu Thr Leu Ser Ser Ile Glu Glu Cys Asp Gln Ile Glu
 1555 1560 1565
 Glu Leu Leu Gly Asp Asp Leu Lys Gly Asp Lys Asp Ala Ser Leu Thr
 1570 1575 1580
 Asp Met Asn Tyr Phe Glu Phe Ser Glu Asp Phe Leu Ala Ser Ile Glu
 1585 1590 1595 1600
 Glu Pro Pro Phe Ala Gly Leu Arg Gly Gly Ser Lys Asn Ile Ala Ile
 1605 1610 1615
 Leu Ala Ile Leu Glu Tyr Ala His Asn Leu Phe Arg Ile Val Ala Ser
 1620 1625 1630
 Lys Cys Ser Lys Arg Pro Leu Phe Leu Ala Phe Ala Glu Leu Ser Ser
 1635 1640 1645
 Ala Leu Ile Glu Lys Phe Lys Glu Val Phe Pro Arg Lys Ser Gln Leu
 1650 1655 1660
 Val Ala Ile Val Arg Glu Tyr Thr Gln Arg Phe Leu Arg Ser Arg Met
 1665 1670 1675 1680
 Arg Ala Leu Gly Leu Asn Asn Glu Phe Val Val Lys Ser Phe Ala Asp
 1685 1690 1695
 Leu Leu Pro Ala Leu Met Lys Arg Lys Val Ser Gly Ser Phe Leu Ala
 1700 1705 1710
 Ser Val Tyr Arg Pro Leu Arg Gly Phe Ser Tyr Met Cys Val Ser Ala
 1715 1720 1725
 Glu Arg Arg Glu Lys Phe Phe Ala Leu Val Cys Leu Ile Gly Leu Ser
 1730 1735 1740
 Leu Pro Phe Phe Val Arg Ile Val Gly Ala Lys Ala Cys Glu Glu Leu
 1745 1750 1755 1760
 Val Ser Ser Ala Arg Arg Phe Tyr Glu Arg Ile Lys Ile Phe Leu Arg
 1765 1770 1775
 Gln Lys Tyr Val Ser Leu Ser Asn Phe Phe Cys His Leu Phe Ser Ser
 1780 1785 1790
 Asp Val Asp Asp Ser Ser Ala Ser Ala Gly Leu Lys Gly Gly Ala Ser
 1795 1800 1805
 Arg Met Thr Leu Phe His Leu Leu Val Arg Leu Ala Ser Ala Leu Leu
 1810 1815 1820
 Ser Leu Gly Trp Glu Gly Leu Lys Leu Leu Leu Ser His His Asn Leu
 1825 1830 1835 1840
 Leu Phe Leu Cys Phe Ala Leu Val Asp Asp Val Asn Val Leu Ile Lys
 1845 1850 1855
 Val Leu Gly Gly Leu Ser Phe Phe Val Gln Pro Ile Phe Ser Leu Phe
 1860 1865 1870

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Ala Ala Met Leu Leu Gln Pro Asp Arg Phe Val Glu Tyr Ser Glu Lys
 1875 1880 1885
 Leu Val Thr Ala Phe Glu Phe Phe Leu Lys Cys Ser Pro Arg Ala Pro
 1890 1895 1900
 Ala Leu Leu Lys Gly Phe Phe Glu Cys Val Ala Asn Ser Thr Val Ser
 1905 1910 1915 1920
 Lys Thr Val Arg Arg Leu Leu Arg Cys Phe Val Lys Met Leu Lys Leu
 1925 1930 1935
 Arg Lys Gly Arg Gly Leu Arg Ala Asp Gly Arg Gly Leu His Arg Gln
 1940 1945 1950
 Lys Ala Val Pro Val Ile Pro Ser Asn Arg Val Val Thr Asp Gly Val
 1955 1960 1965
 Glu Arg Leu Ser Val Lys Met Gln Gly Val Glu Ala Leu Arg Thr Glu
 1970 1975 1980
 Leu Arg Ile Leu Glu Asp Leu Asp Ser Ala Val Ile Glu Lys Leu Asn
 1985 1990 1995 2000
 Arg Arg Arg Asn Arg Asp Thr Asn Asp Asp Glu Phe Thr Arg Pro Ala
 2005 2010 2015
 His Glu Gln Met Gln Glu Val Thr Thr Phe Cys Ser Lys Ala Asn Ser
 2020 2025 2030
 Ala Gly Leu Ala Leu Glu Arg Ala Val Leu Val Glu Asp Ala Ile Lys
 2035 2040 2045
 Ser Glu Lys Leu Ser Lys Thr Val Asn Glu Met Val Arg Lys Gly Ser
 2050 2055 2060
 Thr Thr Ser Glu Glu Val Ala Val Ala Leu Ser Asp Asp Glu Ala Val
 2065 2070 2075 2080
 Glu Glu Ile Ser Val Ala Asp Glu Arg Asp Asp Ser Pro Lys Thr Val
 2085 2090 2095
 Arg Ile Ser Glu Tyr Leu Asn Arg Leu Asn Ser Ser Phe Glu Phe Pro
 2100 2105 2110
 Lys Pro Ile Val Val Asp Asp Asn Lys Asp Thr Gly Gly Leu Thr Asn
 2115 2120 2125
 Ala Val Arg Glu Phe Tyr Tyr Met Gln Glu Leu Ala Leu Phe Glu Ile
 2130 2135 2140
 His Ser Lys Leu Cys Thr Tyr Tyr Asp Gln Leu Arg Ile Val Asn Phe
 2145 2150 2155 2160
 Asp Arg Ser Val Ala Pro Cys Ser Glu Asp Ala Gln Leu Tyr Val Arg
 2165 2170 2175
 Lys Asn Gly Ser Thr Ile Val Gln Gly Lys Glu Val Arg Leu His Ile
 2180 2185 2190

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Lys Asp Phe His Asp His Asp Phe Leu Phe Asp Gly Lys Ile Ser Ile
 2195 2200 2205
 Asn Lys Arg Arg Arg Gly Gly Asn Val Leu Tyr His Asp Asn Leu Ala
 2210 2215 2220
 Phe Leu Ala Ser Asn Leu Phe Leu Ala Gly Tyr Pro Phe Ser Arg Ser
 2225 2230 2235 2240
 Phe Val Phe Thr Asn Ser Ser Val Asp Ile Leu Leu Tyr Glu Ala Pro
 2245 2250 2255
 Pro Gly Gly Gly Lys Thr Thr Thr Leu Ile Asp Ser Phe Leu Lys Val
 2260 2265 2270
 Phe Lys Lys Gly Glu Val Ser Thr Met Ile Leu Thr Ala Asn Lys Ser
 2275 2280 2285
 Ser Gln Val Glu Ile Leu Lys Lys Val Glu Lys Glu Val Ser Asn Ile
 2290 2295 2300
 Glu Cys Gln Lys Arg Lys Asp Lys Arg Ser Pro Lys Lys Ser Ile Tyr
 2305 2310 2315 2320
 Thr Ile Asp Ala Tyr Leu Met His His Arg Gly Cys Asp Ala Asp Val
 2325 2330 2335
 Leu Phe Ile Asp Glu Cys Phe Met Val His Ala Gly Ser Val Leu Ala
 2340 2345 2350
 Cys Ile Glu Phe Thr Arg Cys His Lys Val Met Ile Phe Gly Asp Ser
 2355 2360 2365
 Arg Gln Ile His Tyr Ile Glu Arg Asn Glu Leu Asp Lys Cys Leu Tyr
 2370 2375 2380
 Gly Asp Leu Asp Arg Phe Val Asp Leu Gln Cys Arg Val Tyr Gly Asn
 2385 2390 2395 2400
 Ile Ser Tyr Arg Cys Pro Trp Asp Val Cys Ala Trp Leu Ser Thr Val
 2405 2410 2415
 Tyr Gly Asn Leu Ile Ala Thr Val Lys Gly Glu Ser Glu Gly Lys Ser
 2420 2425 2430
 Ser Met Arg Ile Asn Glu Ile Asn Ser Val Asp Asp Leu Val Pro Asp
 2435 2440 2445
 Val Gly Ser Thr Phe Leu Cys Met Leu Gln Ser Glu Lys Leu Glu Ile
 2450 2455 2460
 Ser Lys His Phe Ile Arg Lys Gly Leu Thr Lys Leu Asn Val Leu Thr
 2465 2470 2475 2480
 Val His Glu Ala Gln Gly Glu Thr Tyr Ala Arg Val Asn Leu Val Arg
 2485 2490 2495
 Leu Lys Phe Gln Glu Asp Glu Pro Phe Lys Ser Ile Arg His Ile Thr
 2500 2505 2510

Val	Ala	Leu	Ser	Arg	His	Thr	Ser	Leu	Thr	Tyr	Asn	Val	Leu	Ala	
		2515						2520					2525		
Ala	Arg	Arg	Gly	Asp	Ala	Thr	Cys	Asp	Ala	Ile	Gln	Lys	Ala	Ala	Glu
		2530					2535					2540			
Leu	Val	Asn	Lys	Phe	Arg	Val	Phe	Pro	Thr	Ser	Phe	Gly	Gly	Ser	Val
		2545				2550					2555				2560
Ile	Asn	Leu	Asn	Val	Lys	Lys	Asp	Val	Glu	Asp	Asn	Ser	Arg	Cys	Lys
				2565						2570				2575	
Ala	Ser	Ser	Ala	Pro	Leu	Ser	Val	Ile	Asn	Asp	Phe	Leu	Asn	Glu	Val
			2580					2585					2590		
Asn	Pro	Gly	Thr	Ala	Val	Ile	Asp	Phe	Gly	Asp	Leu	Ser	Ala	Asp	Phe
		2595					2600					2605			
Ser	Thr	Gly	Pro	Phe	Glu	Cys	Gly	Ala	Ser	Gly	Ile	Val	Val	Arg	Asp
		2610				2615					2620				
Asn	Ile	Ser	Ser	Ser	Asn	Ile	Thr	Asp	His	Asp	Lys	Gln	Arg	Val	
					2630					2635					

and has a molecular weight of about 290 to 300 kDa, preferably 294 kDa.

Another such DNA molecule (GLRaV-2 ORF1b) includes nucleotides 7922-9301 of SEQ. ID. No. 1 and codes for a grapevine leafroll virus RNA-dependent RNA polymerase (RdRP). This DNA molecule comprises the nucleotide sequence corresponding to SEQ. ID. No. 4 as follows:

AGCGTAGTTC	GGTCGCAGGC	GATTCCGCGT	AGAAAACCTT	CTCTACAAGA	AAATTTGTAT	60
TCGTTTGAAG	CGCGGAATTA	TAACTTCTCG	ACTTGCGACC	GTAACACATC	TGCTTCAATG	120
TTCGGAGAGG	CTATGGCGAT	GAAGTGTCTT	CGTCGTTGCT	TCGACCTAGA	TGCCTTTTTCG	180
TCCCTGCGTG	ATGATGTGAT	TAGTATCACA	CGTTCAGGCA	TCGAACAATG	GCTGGAGAAA	240
CGTACTCCTA	GTCAGATTAA	AGCATTAATG	AAGGATGTTG	AATCGCCTTT	GGAAATTGAC	300
GATGAAATTT	GTCGTTTTAA	GTTGATGGTG	AAGCGTGACG	CTAAGGTGAA	GTTAGACTCT	360
TCTTGTTTAA	CTAAACACAG	CGCCGCTCAA	AATATCATGT	TTCATCGCAA	GAGCATTAAT	420
GCTATCTTCT	CTCCTATCTT	TAATGAGGTG	AAAAACCGAA	TAATGTGCTG	TCTTAAGCCT	480
AACATAAAGT	TTTTTACGGA	GATGACTAAC	AGGGATTTTG	CTTCTGTTGT	CAGCAACATG	540
CTTGGTGACG	ACGATGTGTA	CCATATAGGT	GAAGTTGATT	TCTCAAAGTA	CGACAAGTCT	600
CAAGATGCTT	TCGTGAAGGC	TTTTGAAGAA	GTAATGTATA	AGGAACTCGG	TGTTGATGAA	660
GAGTTGCTGG	CTATCTGGAT	GTGCGGCGAG	CGGTTATCGA	TAGCTAACAC	TCTCGATGGT	720
CAGTTGTCCT	TCACGATCGA	GAATCAAAGG	AAGTCGGGAG	CTTCAACAC	TTGGATTGGT	780

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AACTCTCTCG TCACTTTGGG TATTTTAAGT CTTTACTACG ACGTTAGAAA TTTCGAGGCG      840
TTGTACATCT CGGGCGATGA TTCTTTAATT TTTTCTCGCA GCGAGATTTC GAATTATGCC      900
GACGACATAT GCACTGACAT GGGTTTTGAG ACAAATTTA TGTCCCCAAG TGTCCCGTAC      960
TTTTGTTCTA AATTTGTTGT TATGTGTGGT CATAAGACGT TTTTGTTC CGACCCGTAC     1020
AAGCTTTTTG TCAAGTTGGG AGCAGTCAAA GAGGATGTTT CAATGGATTT CCTTTTCGAG     1080
ACTTTTACCT CCTTTAAAGA CTTAACCTCC GATTTTAACG ACGAGCGCTT AATTCAAAG      1140
CTCGCTGAAC TTGTGGCTTT AAAATATGAG GTTCAAACCG GCAACACCAC CTTGGCGTTA     1200
AGTGTGATAC ATTGTTTGCG TTCGAATTC CTCTCGTTTA GCAAGTTATA TCCTCGCGTG     1260
AAGGGATGGC AGGTTTTTTA CACGTCGGTT AAGAAAGCGC TTCTCAAGAG TGGGTGTTCT     1320
CTCTTCGACA GTTTCATGAC CCCTTTTGGT CAGGCTGTCA TGGTTTGGGA TGATGAGTAG     1380

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The RNA-dependent RNA polymerase has an amino acid sequence corresponding to SEQ. ID. No. 5 as follows:

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Ser Val Val Arg Ser Gln Ala Ile Pro Arg Arg Lys Pro Ser Leu Gln
1           5           10           15
Glu Asn Leu Tyr Ser Phe Glu Ala Arg Asn Tyr Asn Phe Ser Thr Cys
20          25          30
Asp Arg Asn Thr Ser Ala Ser Met Phe Gly Glu Ala Met Ala Met Asn
35          40          45
Cys Leu Arg Arg Cys Phe Asp Leu Asp Ala Phe Ser Ser Leu Arg Asp
50          55          60
Asp Val Ile Ser Ile Thr Arg Ser Gly Ile Glu Gln Trp Leu Glu Lys
65          70          75          80
Arg Thr Pro Ser Gln Ile Lys Ala Leu Met Lys Asp Val Glu Ser Pro
85          90          95
Leu Glu Ile Asp Asp Glu Ile Cys Arg Phe Lys Leu Met Val Lys Arg
100         105         110
Asp Ala Lys Val Lys Leu Asp Ser Ser Cys Leu Thr Lys His Ser Ala
115         120         125
Ala Gln Asn Ile Met Phe His Arg Lys Ser Ile Asn Ala Ile Phe Ser
130         135         140
Pro Ile Phe Asn Glu Val Lys Asn Arg Ile Met Cys Cys Leu Lys Pro
145         150         155         160
Asn Ile Lys Phe Phe Thr Glu Met Thr Asn Arg Asp Phe Ala Ser Val
165         170         175
Val Ser Asn Met Leu Gly Asp Asp Asp Val Tyr His Ile Gly Glu Val
180         185         190

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Asp	Phe	Ser	Lys	Tyr	Asp	Lys	Ser	Gln	Asp	Ala	Phe	Val	Lys	Ala	Phe		
		195					200					205					
Glu	Glu	Val	Met	Tyr	Lys	Glu	Leu	Gly	Val	Asp	Glu	Glu	Leu	Leu	Ala		
	210					215				220							
Ile	Trp	Met	Cys	Gly	Glu	Arg	Leu	Ser	Ile	Ala	Asn	Thr	Leu	Asp	Gly		
225					230					235					240		
Gln	Leu	Ser	Phe	Thr	Ile	Glu	Asn	Gln	Arg	Lys	Ser	Gly	Ala	Ser	Asn		
				245					250					255			
Thr	Trp	Ile	Gly	Asn	Ser	Leu	Val	Thr	Leu	Gly	Ile	Leu	Ser	Leu	Tyr		
			260					265					270				
Tyr	Asp	Val	Arg	Asn	Phe	Glu	Ala	Leu	Tyr	Ile	Ser	Gly	Asp	Asp	Ser		
		275					280					285					
Leu	Ile	Phe	Ser	Arg	Ser	Glu	Ile	Ser	Asn	Tyr	Ala	Asp	Asp	Ile	Cys		
	290					295					300						
Thr	Asp	Met	Gly	Phe	Glu	Thr	Lys	Phe	Met	Ser	Pro	Ser	Val	Pro	Tyr		
305					310					315					320		
Phe	Cys	Ser	Lys	Phe	Val	Val	Met	Cys	Gly	His	Lys	Thr	Phe	Phe	Val		
				325					330					335			
Pro	Asp	Pro	Tyr	Lys	Leu	Phe	Val	Lys	Leu	Gly	Ala	Val	Lys	Glu	Asp		
			340					345					350				
Val	Ser	Met	Asp	Phe	Leu	Phe	Glu	Thr	Phe	Thr	Ser	Phe	Lys	Asp	Leu		
		355					360					365					
Thr	Ser	Asp	Phe	Asn	Asp	Glu	Arg	Leu	Ile	Gln	Lys	Leu	Ala	Glu	Leu		
	370					375					380						
Val	Ala	Leu	Lys	Tyr	Glu	Val	Gln	Thr	Gly	Asn	Thr	Thr	Leu	Ala	Leu		
385					390					395					400		
Ser	Val	Ile	His	Cys	Leu	Arg	Ser	Asn	Phe	Leu	Ser	Phe	Ser	Lys	Leu		
				405					410					415			
Tyr	Pro	Arg	Val	Lys	Gly	Trp	Gln	Val	Phe	Tyr	Thr	Ser	Val	Lys	Lys		
			420				425						430				
Ala	Leu	Leu	Lys	Ser	Gly	Cys	Ser	Leu	Phe	Asp	Ser	Phe	Met	Thr	Pro		
		435					440					445					
Phe	Gly	Gln	Ala	Val	Met	Val	Trp	Asp	Asp	Glu							
	450					455											

and a molecular weight from about 50 to about 54 kDa, preferably about 52 kDa.

Another such DNA molecule (GLRAV-2 ORF2) includes nucleotides 9365-9535 of SEQ. ID. No. 1 and codes for a small, grapevine leafroll virus hydrophobic protein or polypeptide. This DNA molecule comprises the nucleotide sequence

5 corresponding to SEQ. ID. No. 6 as follows:

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ATGAATCAGG TTTTGCAGTT TGAATGTTTG TTTCTGCTGA ATCTCGCGGT TTTTGCTGTG 60
 ACTTTCATTT TCATTCTTCT GGTCTTCCGC GTGATTAAGT CTTTTCGCCA GAAGGGTCAC 120
 GAAGCACCTG TTCCCGTTGT TCGTGGCGGG GGTTTTTCAA CCGTAGTGTA G 171

The small hydrophobic protein or polypeptide has an amino acid sequence corresponding to SEQ. ID. No. 7 as follows:

Met	Asn	Gln	Val	Leu	Gln	Phe	Glu	Cys	Leu	Phe	Leu	Leu	Asn	Leu	Ala
1				5					10					15	
Val	Phe	Ala	Val	Thr	Phe	Ile	Phe	Ile	Leu	Leu	Val	Phe	Arg	Val	Ile
			20					25					30		
Lys	Ser	Phe	Arg	Gln	Lys	Gly	His	Glu	Ala	Pro	Val	Pro	Val	Val	Arg
		35					40					45			
Gly	Gly	Gly	Phe	Ser	Thr	Val	Val								
	50					55									

and a molecular weight from about 5 to about 7 kDa, preferably about 6 kDa.

Another such DNA molecule (GLRaV-2 ORF3) includes nucleotides
 5 9551-11350 of SEQ. ID. No. 1 and encodes for a grapevine leafroll virus heat shock 70
 protein. This DNA molecule comprises the nucleotide sequence corresponding to SEQ.
 ID. No. 8 as follows:

ATGGTAGTTT TCGGTTTGGA CTTTGGCACC ACATTCTCTA CGGTGTGTGT GTACAAGGAT 60
 GGACGAGTTT TTTCATTCAA GCAGAATAAT TCGGCGTACA TCCCCACTTA CCTCTATCTC 120
 TTCTCCGATT CTAACCACAT GACTTTTGGT TACGAGGCCG AATCACTGAT GAGTAATCTG 180
 AAAGTTAAAG GTTCGTTTTA TAGAGATTTA AAACGTTGGG TGGGTGCGA TTCGAGTAAC 240
 CTCGACGCGT ACCTTGACCG TTTAAAACCT CATTACTCGG TCCGCTTGGT TAAGATCGGC 300
 TCTGGCTTGA ACGAACTGT TTCAATTGGA AACTTCGGGG GCACTGTAA GTCTGAGGCT 360
 CATCTGCCAG GGTGATAGC TCTCTTTATT AAGGCTGTCA TTAGTTGCGC GGAGGGCGCG 420
 TTTGCGTGCA CTTGCACCGG GGTTATTTGT TCAGTACCTG CCAATTATGA TAGCGTTCAA 480
 AGGAATTTCA CTGATCAGTG TGTTTCACTC AGCGGTTATC AGTGCGTATA TATGATCAAT 540
 GAACCTTCAG CGGCTGCGCT ATCTGCGTGT AATTCGATTG GAAAGAAGTC CGCAAATTTG 600
 GCTGTTTACG ATTTGCGTGG TGGGACCTTC GACGTGTCTA TCATTTTATA CCGCAACAAT 660
 ACTTTTGTTG TGCGAGCTTC TGGAGGCGAT CTAAATCTCG GTGGAAGGGA TGTTGATCGT 720
 GCGTTTCTCA CGCACCTCTT CTCTTTAACA TCGCTGGAAC CTGACCTCAC TTTGGATATC 780

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TCGAATCTGA AAGAATCTTT ATCAAAAACG GACGCAGAGA TAGTTTACAC TTTGAGAGGT      840
GTCGATGGAA GAAAAGAAGA CGTTAGAGTA AACAAAAACA TTCTTACGTC GGTGATGCTC      900
CCCTACGTGA ACAGAACGCT TAAGATATTA GAGTCAACCT TAAAATCGTA TGCTAAGAGT      960
ATGAATGAGA GTGCGCGAGT TAAGTGCGAT TTAGTGCTGA TAGGAGGATC TTCATATCTT     1020
CCTGGCCTGG CAGACGTACT AACGAAGCAT CAGAGCGTTG ATCGTATCTT AAGAGTTTCG     1080
GATCCTCGGG CTGCCGTGGC CGTCGGTTGC GCATTATATT CTTCATGCCT CTCAGGATCT     1140
GGGGGGTTGC TACTGATCGA CTGTGCAGCT CACACTGTGC CTATAGCGGA CAGAAGTTGT     1200
CATCAAATCA TTTGCGCTCC AGCGGGGGCA CCGATCCCCT TTTCAGGAAG CATGCCTTTG     1260
TACTTAGCCA GGGTCAACAA GAACTCGCAG CGTGAAGTCG CCGTGTTTGA AGGGGAGTAC     1320
GTTAAGTGCC CTAAGAACAG AAAGATCTGT GGAGCAAATA TAAGATTTTT TGATATAGGA     1380
GTGACGGGTG ATTCGTACGC ACCCGTTACC TTCTATATGG ATTTCTCCAT TTCAAGCGTA     1440
GGAGCCGTTT CATTCGTGGT GAGAGGTCCT GAGGGTAAGC AAGTGTCACT CACTGGAAct     1500
CCAGCGTATA ACTTTTCGTC TGTGGCTCTC GGATCACGCA GTGTCCGAGA ATTGCATATT     1560
AGTTTAAATA ATAAAGTTTT TCTCGGTTTG CTTCTACATA GAAAGGCGGA TCGACGAATA     1620
CTTTTCACTA AGGATGAAGC GATTTCGATAC GCCGATTCAA TTGATATCGC GGATGTGCTA     1680
AAGGAATATA AAAGTTACGC GGCCAGTGCC TTACCACCAG ACGAGGATGT CGAATTACTC     1740
CTGGGAAAGT CTGTTCAAAA AGTTTTACGG GGAAGCAGAC TGGAAGAAAT ACCTCTCTAG     1800

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The heat shock 70 protein is believed to function as a chaperone protein and has an amino acid sequence corresponding to SEQ. ID. No. 9 as follows:

```

Met Val Val Phe Gly Leu Asp Phe Gly Thr Thr Phe Ser Thr Val Cys
1           5           10           15

Val Tyr Lys Asp Gly Arg Val Phe Ser Phe Lys Gln Asn Asn Ser Ala
          20           25           30

Tyr Ile Pro Thr Tyr Leu Tyr Leu Phe Ser Asp Ser Asn His Met Thr
          35           40           45

Phe Gly Tyr Glu Ala Glu Ser Leu Met Ser Asn Leu Lys Val Lys Gly
          50           55           60

Ser Phe Tyr Arg Asp Leu Lys Arg Trp Val Gly Cys Asp Ser Ser Asn
65           70           75           80

Leu Asp Ala Tyr Leu Asp Arg Leu Lys Pro His Tyr Ser Val Arg Leu
          85           90           95

Val Lys Ile Gly Ser Gly Leu Asn Glu Thr Val Ser Ile Gly Asn Phe
          100          105          110

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Gly Gly Thr Val Lys Ser Glu Ala His Leu Pro Gly Leu Ile Ala Leu
 115 120 125
 Phe Ile Lys Ala Val Ile Ser Cys Ala Glu Gly Ala Phe Ala Cys Thr
 130 135 140
 Cys Thr Gly Val Ile Cys Ser Val Pro Ala Asn Tyr Asp Ser Val Gln
 145 150 155 160
 Arg Asn Phe Thr Asp Gln Cys Val Ser Leu Ser Gly Tyr Gln Cys Val
 165 170 175
 Tyr Met Ile Asn Glu Pro Ser Ala Ala Ala Leu Ser Ala Cys Asn Ser
 180 185 190
 Ile Gly Lys Lys Ser Ala Asn Leu Ala Val Tyr Asp Phe Gly Gly Gly
 195 200 205
 Thr Phe Asp Val Ser Ile Ile Ser Tyr Arg Asn Asn Thr Phe Val Val
 210 215 220
 Arg Ala Ser Gly Gly Asp Leu Asn Leu Gly Gly Arg Asp Val Asp Arg
 225 230 235 240
 Ala Phe Leu Thr His Leu Phe Ser Leu Thr Ser Leu Glu Pro Asp Leu
 245 250 255
 Thr Leu Asp Ile Ser Asn Leu Lys Glu Ser Leu Ser Lys Thr Asp Ala
 260 265 270
 Glu Ile Val Tyr Thr Leu Arg Gly Val Asp Gly Arg Lys Glu Asp Val
 275 280 285
 Arg Val Asn Lys Asn Ile Leu Thr Ser Val Met Leu Pro Tyr Val Asn
 290 295 300
 Arg Thr Leu Lys Ile Leu Glu Ser Thr Leu Lys Ser Tyr Ala Lys Ser
 305 310 315 320
 Met Asn Glu Ser Ala Arg Val Lys Cys Asp Leu Val Leu Ile Gly Gly
 325 330 335
 Ser Ser Tyr Leu Pro Gly Leu Ala Asp Val Leu Thr Lys His Gln Ser
 340 345 350
 Val Asp Arg Ile Leu Arg Val Ser Asp Pro Arg Ala Ala Val Ala Val
 355 360 365
 Gly Cys Ala Leu Tyr Ser Ser Cys Leu Ser Gly Ser Gly Gly Leu Leu
 370 375 380
 Leu Ile Asp Cys Ala Ala His Thr Val Ala Ile Ala Asp Arg Ser Cys
 385 390 395 400
 His Gln Ile Ile Cys Ala Pro Ala Gly Ala Pro Ile Pro Phe Ser Gly
 405 410 415
 Ser Met Pro Leu Tyr Leu Ala Arg Val Asn Lys Asn Ser Gln Arg Glu
 420 425 430

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Val	Ala	Val	Phe	Glu	Gly	Glu	Tyr	Val	Lys	Cys	Pro	Lys	Asn	Arg	Lys	
		435					440					445				
Ile	Cys	Gly	Ala	Asn	Ile	Arg	Phe	Phe	Asp	Ile	Gly	Val	Thr	Gly	Asp	
	450					455					460					
Ser	Tyr	Ala	Pro	Val	Thr	Phe	Tyr	Met	Asp	Phe	Ser	Ile	Ser	Ser	Val	
465					470					475					480	
Gly	Ala	Val	Ser	Phe	Val	Val	Arg	Gly	Pro	Glu	Gly	Lys	Gln	Val	Ser	
				485					490					495		
Leu	Thr	Gly	Thr	Pro	Ala	Tyr	Asn	Phe	Ser	Ser	Val	Ala	Leu	Gly	Ser	
			500					505					510			
Arg	Ser	Val	Arg	Glu	Leu	His	Ile	Ser	Leu	Asn	Asn	Lys	Val	Phe	Leu	
		515					520					525				
Gly	Leu	Leu	Leu	His	Arg	Lys	Ala	Asp	Arg	Arg	Ile	Leu	Phe	Thr	Lys	
	530					535					540					
Asp	Glu	Ala	Ile	Arg	Tyr	Ala	Asp	Ser	Ile	Asp	Ile	Ala	Asp	Val	Leu	
545					550					555					560	
Lys	Glu	Tyr	Lys	Ser	Tyr	Ala	Ala	Ser	Ala	Leu	Pro	Pro	Asp	Glu	Asp	
				565					570					575		
Val	Glu	Leu	Leu	Leu	Gly	Lys	Ser	Val	Gln	Lys	Val	Leu	Arg	Gly	Ser	
			580					585					590			
Arg	Leu	Glu	Glu	Ile	Pro	Leu										
			595													

and a molecular weight from about 63 to about 67 kDa, preferably about 65 kDa.

Another such DNA molecule (GLRaV-2 ORF4) includes nucleotides 11277-12932 of SEQ. ID. No. 1 and codes for a putative grapevine leafroll virus heat shock 90 protein. This DNA molecule comprises a nucleotide sequence corresponding to

5 SEQ. ID. No. 10 as follows:

ATGTCGAATT ACTCCTGGGA AAGTCTGTTC AAAAAGTTTT ACGGGGAAGC AGACTGGAAG	60
AAATACCTCT CTAGGAGCAT AGCAGCACAC TCAAGTGAAA TTAAACTCT ACCAGACATT	120
CGATTGTACG GCGGTAGGGT TGTAAAGAAG TCCGAATTCG AATCAGCACT TCCTAATTCT	180
TTTGAACAGG AATTAGGACT GTTCATACTG AGCGAACGGG AAGTGGGATG GAGCAAATTA	240
TGCGGAATAA CGGTGGAAGA AGCAGCATAC GATCTTACGA ATCCCAAGGC TTATAAATTC	300
ACTGCCGAGA CATGTAGCCC GGATGTAAAA GGTGAAGGAC AAAAATACTC TATGGAAGAC	360
GTGATGAATT TCATGCGTTT ATCAAATCTG GATGTTAACG ACAAGATGCT GACGGAACAG	420
TGTTGGTCGC TGTCCAATTC ATGCGGTGAA TTGATCAACC CAGACGACAA AGGGCGATTC	480
GTGGCTCTCA CCTTTAAGGA CAGAGACACA GCTGATGACA CGGGTGCCGC CAACGTGGAA	540

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TGTCGCGTGG GCGACTATCT AGTTTACGCT ATGTCCCTGT TTGAGCAGAG GACCCAAAAA    600
TCGCAGTCTG GCAACATCTC TCTGTACGAA AAGTACTGTG AATACATCAG GACCTACTTA    660
GGGAGTACAG ACCTGTTCTT CACAGCGCCG GACAGGATTC CGTTACTTAC GGGCATCCTA    720
TACGATTTTT GTAAGGAATA CAACGTTTTT TACTCGTCAT ATAAGAGAAA CGTCGATAAT    780
TTCAGATTCT TCTTGGCGAA TTATATGCCT TTGATATCTG ACGTCTTTGT CTTCCAGTGG    840
GTAAAACCCG CGCCGGATGT TCGGCTGCTT TTTGAGTTAA GTGCAGCGGA ACTAACGCTG    900
GAGGTTCCCA CACTGAGTTT GATAGATTCT CAAGTTGTGG TAGGTCATAT CTTAAGATAC    960
GTAGAATCCT ACACATCAGA TCCAGCCATC GACGCGTTAG AAGACAAACT GGAAGCGATA   1020
CTGAAAAGTA GCAATCCCCG TCTATCGACA GCGCAACTAT GGGTTGGTTT CTTTTGTTAC   1080
TATGGTGAGT TTCGTACGGC TCAAAGTAGA GTAGTGCAAA GACCAGGCGT ATACAAAACA   1140
CCTGACTCAG TGGGTGGATT TGAAATAAAC ATGAAAGATG TTGAGAAATT CTTGATAAAA   1200
CTTCAGAGAG AATTGCCTAA TGTATCTTTG CGGCGTCAGT TTAACGGAGC TAGAGCGCAT   1260
GAGGCTTTCA AAATATTTAA AAACGGAAAT ATAAGTTTCA GACCTATATC GCGTTTAAAC   1320
GTGCCTAGAG AGTTCTGGTA TCTGAACATA GACTACTTCA GGCACGCGAA TAGGTCCGGG   1380
TTAACCGAAG AAGAAATACT CATCCTAAAC AACATAAGCG TTGATGTTAG GAAGTTATGC   1440
GCTGAGAGAG CGTGCAATAC CCTACCTAGC GCGAAGCGCT TTAGTAAAAA TCATAAGAGT   1500
AATATACAAT CATCAGCCA AGAGCGGAGG ATTAAAGACC CATTGGTAGT CCTGAAAGAC   1560
ACTTTATATG AGTTCCAACA CAAGCGTGCC GGTGGGGGT CTCGAAGCAC TCGAGACCTC   1620
GGGAGTCGTG CTGACCACGC GAAAGGAAGC GGTGTA                               1656

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The heat shock 90 protein has an amino acid sequence corresponding to SEQ. ID. No. 11 as follows:

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Met Ser Asn Tyr Ser Trp Glu Ser Leu Phe Lys Lys Phe Tyr Gly Glu
1           5           10           15

Ala Asp Trp Lys Lys Tyr Leu Ser Arg Ser Ile Ala Ala His Ser Ser
          20           25           30

Glu Ile Lys Thr Leu Pro Asp Ile Arg Leu Tyr Gly Gly Arg Val Val
          35           40           45

Lys Lys Ser Glu Phe Glu Ser Ala Leu Pro Asn Ser Phe Glu Gln Glu
          50           55           60

Leu Gly Leu Phe Ile Leu Ser Glu Arg Glu Val Gly Trp Ser Lys Leu
65           70           75           80

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Cys Gly Ile Thr Val Glu Glu Ala Ala Tyr Asp Leu Thr Asn Pro Lys
 85 90 95
 Ala Tyr Lys Phe Thr Ala Glu Thr Cys Ser Pro Asp Val Lys Gly Glu
 100 105 110
 Gly Gln Lys Tyr Ser Met Glu Asp Val Met Asn Phe Met Arg Leu Ser
 115 120 125
 Asn Leu Asp Val Asn Asp Lys Met Leu Thr Glu Gln Cys Trp Ser Leu
 130 135 140
 Ser Asn Ser Cys Gly Glu Leu Ile Asn Pro Asp Asp Lys Gly Arg Phe
 145 150 155 160
 Val Ala Leu Thr Phe Lys Asp Arg Asp Thr Ala Asp Asp Thr Gly Ala
 165 170 175
 Ala Asn Val Glu Cys Arg Val Gly Asp Tyr Leu Val Tyr Ala Met Ser
 180 185 190
 Leu Phe Glu Gln Arg Thr Gln Lys Ser Gln Ser Gly Asn Ile Ser Leu
 195 200 205
 Tyr Glu Lys Tyr Cys Glu Tyr Ile Arg Thr Tyr Leu Gly Ser Thr Asp
 210 215 220
 Leu Phe Phe Thr Ala Pro Asp Arg Ile Pro Leu Leu Thr Gly Ile Leu
 225 230 235 240
 Tyr Asp Phe Cys Lys Glu Tyr Asn Val Phe Tyr Ser Ser Tyr Lys Arg
 245 250 255
 Asn Val Asp Asn Phe Arg Phe Phe Leu Ala Asn Tyr Met Pro Leu Ile
 260 265 270
 Ser Asp Val Phe Val Phe Gln Trp Val Lys Pro Ala Pro Asp Val Arg
 275 280 285
 Leu Leu Phe Glu Leu Ser Ala Ala Glu Leu Thr Leu Glu Val Pro Thr
 290 295 300
 Leu Ser Leu Ile Asp Ser Gln Val Val Val Gly His Ile Leu Arg Tyr
 305 310 315 320
 Val Glu Ser Tyr Thr Ser Asp Pro Ala Ile Asp Ala Leu Glu Asp Lys
 325 330 335
 Leu Glu Ala Ile Leu Lys Ser Ser Asn Pro Arg Leu Ser Thr Ala Gln
 340 345 350
 Leu Trp Val Gly Phe Phe Cys Tyr Tyr Gly Glu Phe Arg Thr Ala Gln
 355 360 365
 Ser Arg Val Val Gln Arg Pro Gly Val Tyr Lys Thr Pro Asp Ser Val
 370 375 380
 Gly Gly Phe Glu Ile Asn Met Lys Asp Val Glu Lys Phe Phe Asp Lys
 385 390 395 400

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Leu	Gln	Arg	Glu	Leu	Pro	Asn	Val	Ser	Leu	Arg	Arg	Gln	Phe	Asn	Gly	
				405					410					415		
Ala	Arg	Ala	His	Glu	Ala	Phe	Lys	Ile	Phe	Lys	Asn	Gly	Asn	Ile	Ser	
			420					425					430			
Phe	Arg	Pro	Ile	Ser	Arg	Leu	Asn	Val	Pro	Arg	Glu	Phe	Trp	Tyr	Leu	
		435					440					445				
Asn	Ile	Asp	Tyr	Phe	Arg	His	Ala	Asn	Arg	Ser	Gly	Leu	Thr	Glu	Glu	
	450					455					460					
Glu	Ile	Leu	Ile	Leu	Asn	Asn	Ile	Ser	Val	Asp	Val	Arg	Lys	Leu	Cys	
465					470					475					480	
Ala	Glu	Arg	Ala	Cys	Asn	Thr	Leu	Pro	Ser	Ala	Lys	Arg	Phe	Ser	Lys	
				485					490					495		
Asn	His	Lys	Ser	Asn	Ile	Gln	Ser	Ser	Arg	Gln	Glu	Arg	Arg	Ile	Lys	
			500					505					510			
Asp	Pro	Leu	Val	Val	Leu	Lys	Asp	Thr	Leu	Tyr	Glu	Phe	Gln	His	Lys	
		515					520					525				
Arg	Ala	Gly	Trp	Gly	Ser	Arg	Ser	Thr	Arg	Asp	Leu	Gly	Ser	Arg	Ala	
	530					535					540					
Asp	His	Ala	Lys	Gly	Ser	Gly										
545					550											

and a molecular weight from about 61 to about 65 kDa, preferably about 63 kDa.

Yet another DNA molecule of the present invention (GLRaV-2 ORF5) includes nucleotides 12844-13515 of SEQ. ID. No. 1 and codes for a diverged coat protein. This DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID.

5 No. 12 as follows:

ATGAGTTCCA	ACACAAGCGT	GCCGGTTGGG	GGTCTCGAAG	CACTCGAGAC	CTCGGGAGTC	60
GTGCTGACCA	CGCGAAAGGA	AGCGGTTGAT	AAGTTTTTTA	ATGAACTAAA	AAACGAAAAT	120
TACTCATCAG	TTGACAGCAG	CCGATTAAGC	GATTCGGAAG	TAAAAGAAGT	GTTAGAGAAA	180
AGTAAAGAAA	GTTTCAAAAG	CGAACTGGCC	TCCACTGACG	AGCACTTCGT	CTACCACATT	240
ATATTTTTCT	TAATCCGATG	TGCTAAGATA	TCGACAAGTG	AAAAGGTGAA	GTACGTTGGT	300
AGTCATACGT	ACGTGGTCGA	CGGAAAAACG	TACACCGTTC	TTGACGCTTG	GGTATTCAAC	360
ATGATGAAAA	GTCTACGAA	GAAGTACAAA	CGAGTGAATG	GTCTGCGTGC	GTTCTGTTGC	420
GCGTGCGAAG	ATCTATATCT	AACCGTCGCA	CCAATAATGT	CAGAACGCTT	TAAGACTAAA	480
GCCGTAGGGA	TGAAAGGTTT	GCCTGTTGGA	AAGGAATACT	TAGGCGCCGA	CTTTCTTTTCG	540
GGAAC TAGCA	AACTGATGAG	CGATCACGAC	AGGGCGGTCT	CCATCGTTGC	AGCGAAAAAC	600

GCTGTCGATC GTAGCGCTTT CACGGGTGGG GAGAGAAAGA TAGTTAGTTT GTATGATCTA 660
 GGGAGGTACT AA 672

The diverged coat protein has an amino acid sequence corresponding to SEQ. ID. No. 13 as follows:

Met	Ser	Ser	Asn	Thr	Ser	Val	Pro	Val	Gly	Gly	Leu	Glu	Ala	Leu	Glu	1	5	10	15
Thr	Ser	Gly	Val	Val	Leu	Thr	Thr	Arg	Lys	Glu	Ala	Val	Asp	Lys	Phe	20	25	30	
Phe	Asn	Glu	Leu	Lys	Asn	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ser	Ser	Arg	35	40	45	
Leu	Ser	Asp	Ser	Glu	Val	Lys	Glu	Val	Leu	Glu	Lys	Ser	Lys	Glu	Ser	50	55	60	
Phe	Lys	Ser	Glu	Leu	Ala	Ser	Thr	Asp	Glu	His	Phe	Val	Tyr	His	Ile	65	70	75	80
Ile	Phe	Phe	Leu	Ile	Arg	Cys	Ala	Lys	Ile	Ser	Thr	Ser	Glu	Lys	Val	85	90	95	
Lys	Tyr	Val	Gly	Ser	His	Thr	Tyr	Val	Val	Asp	Gly	Lys	Thr	Tyr	Thr	100	105	110	
Val	Leu	Asp	Ala	Trp	Val	Phe	Asn	Met	Met	Lys	Ser	Leu	Thr	Lys	Lys	115	120	125	
Tyr	Lys	Arg	Val	Asn	Gly	Leu	Arg	Ala	Phe	Cys	Cys	Ala	Cys	Glu	Asp	130	135	140	
Leu	Tyr	Leu	Thr	Val	Ala	Pro	Ile	Met	Ser	Glu	Arg	Phe	Lys	Thr	Lys	145	150	155	160
Ala	Val	Gly	Met	Lys	Gly	Leu	Pro	Val	Gly	Lys	Glu	Tyr	Leu	Gly	Ala	165	170	175	
Asp	Phe	Leu	Ser	Gly	Thr	Ser	Lys	Leu	Met	Ser	Asp	His	Asp	Arg	Ala	180	185	190	
Val	Ser	Ile	Val	Ala	Ala	Lys	Asn	Ala	Val	Asp	Arg	Ser	Ala	Phe	Thr	195	200	205	
Gly	Gly	Glu	Arg	Lys	Ile	Val	Ser	Leu	Tyr	Asp	Leu	Gly	Arg	Tyr	210	215	220		

and a molecular weight from about 23 to about 27 kDa, preferably about 25 kDa.

Another such DNA molecule (GLRaV-2 ORF6) includes nucleotides
 5 13584-14180 of SEQ. ID. No. 1 and codes for a grapevine leafroll virus coat protein.
 This DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 14
 as follows:

```

ATGGAGTTGA TGTCCGACAG CAACCTTAGC AACCTGGTGA TAACCGACGC CTCTAGTCTA      60
AATGGTGTCTG ACAAGAAGCT TTTATCTGCT GAAGTTGAAA AAATGTTGGT GCAGAAAGGG      120
GCTCCTAACG AGGGTATAGA AGTGGTGTTT GGTCTACTCC TTTACGCACT CGCGGCAAGA      180
ACCACGTCTC CTAAGGTTCA GCGCGCAGAT TCAGACGTTA TATTTTCAAA TAGTTTCGGA      240
GAGAGGAATG TGGTAGTAAC AGAGGGTGAC CTTAAGAAGG TACTCGACGG GTGTGCGCCT      300
CTCACTAGGT TCACTAATAA ACTTAGAACG TTCGGTCGTA CTTTCACTGA GGCTTACGTT      360
GACTTTTGTA TCGCGTATAA GCACAAATTA CCCCAACTCA ACGCCGCGGC GGAATTGGGG      420
ATTCCAGCTG AAGATTCGTA CTTAGCTGCA GATTTTCTGG GTACTTGCCC GAAGCTCTCT      480
GAATTACAGC AAAGTAGGAA GATGTTTCGCG AGTATGTACG CTCTAAAAAC TGAAGGTGGA      540
GTGGTAAATA CACCAGTGAG CAATCTGCGT CAGCTAGGTA GAAGGGAAGT TATGTAA      597

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The coat protein has an amino acid sequence corresponding to SEQ. ID. No. 15 as follows:

```

Met Glu Leu Met Ser Asp Ser Asn Leu Ser Asn Leu Val Ile Thr Asp
1           5           10           15
Ala Ser Ser Leu Asn Gly Val Asp Lys Lys Leu Leu Ser Ala Glu Val
20          25          30
Glu Lys Met Leu Val Gln Lys Gly Ala Pro Asn Glu Gly Ile Glu Val
35          40          45
Val Phe Gly Leu Leu Leu Tyr Ala Leu Ala Ala Arg Thr Thr Ser Pro
50          55          60
Lys Val Gln Arg Ala Asp Ser Asp Val Ile Phe Ser Asn Ser Phe Gly
65          70          75          80
Glu Arg Asn Val Val Val Thr Glu Gly Asp Leu Lys Lys Val Leu Asp
85          90          95
Gly Cys Ala Pro Leu Thr Arg Phe Thr Asn Lys Leu Arg Thr Phe Gly
100         105         110
Arg Thr Phe Thr Glu Ala Tyr Val Asp Phe Cys Ile Ala Tyr Lys His
115        120        125
Lys Leu Pro Gln Leu Asn Ala Ala Ala Glu Leu Gly Ile Pro Ala Glu
130        135        140
Asp Ser Tyr Leu Ala Ala Asp Phe Leu Gly Thr Cys Pro Lys Leu Ser
145        150        155        160
Glu Leu Gln Gln Ser Arg Lys Met Phe Ala Ser Met Tyr Ala Leu Lys
165        170        175

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Thr Glu Gly Gly Val Val Asn Thr Pro Val Ser Asn Leu Arg Gln Leu
 180 185 190

Gly Arg Arg Glu Val Met
 195

and a molecular weight from about 20 to about 24 kDa, preferably about 22 kDa.

Another such DNA molecule (GLRaV-2 ORF7) includes nucleotides 14180-14665 of SEQ. ID. No. 1 and codes for a second undefined grapevine leafroll virus protein or polypeptide. This DNA molecule comprises a nucleotide sequence

5 corresponding to SEQ. ID. No. 16 as follows:

ATGGAAGATT ACGAAGAAAA ATCCGAATCG CTCATACTGC TACGCACGAA TCTGAACACT 60

ATGCTTTT TAG TGGTCAAGTC CGATGCTAGT GTAGAGCTGC CTAAACTACT AATTTGCGGT 120

TACTTACGAG TGTCAGGACG TGGGGAGGTG ACGTGTTCGA ACCGTGAGGA ATTAACAAGA 180

GATTTTGAGG GCAATCATCA TACGGTGATC CGTTCTAGAA TCATACAATA TGACAGCGAG 240

TCTGCTTTTG AGGAATTCAA CAACTCTGAT TGCGTAGTGA AGTTTTTCCT AGAGACTGGT 300

AGTGTCTTTT GGTTTTTCCT TCGAAGTGAA ACCAAAGGTA GAGCGGTGCG ACATTTGCGC 360

ACCTTCTTCG AAGCTAACAA TTTCTTCTTT GGATCGCATT GCGGTACCAT GGAGTATTGT 420

TTGAAGCAGG TACTAACTGA AACTGAATCT ATAATCGATT CTTTTTGCGA AGAAAGAAAT 480

CGTTAA 486

The second undefined grapevine leafroll virus protein or polypeptide has a deduced amino acid sequence corresponding to SEQ. ID. No. 17 as follows:

Met Glu Asp Tyr Glu Glu Lys Ser Glu Ser Leu Ile Leu Leu Arg Thr
 1 5 10 15

Asn Leu Asn Thr Met Leu Leu Val Val Lys Ser Asp Ala Ser Val Glu
 20 25 30

Leu Pro Lys Leu Leu Ile Cys Gly Tyr Leu Arg Val Ser Gly Arg Gly
 35 40 45

Glu Val Thr Cys Cys Asn Arg Glu Glu Leu Thr Arg Asp Phe Glu Gly
 50 55 60

Asn His His Thr Val Ile Arg Ser Arg Ile Ile Gln Tyr Asp Ser Glu
 65 70 75 80

Ser Ala Phe Glu Glu Phe Asn Asn Ser Asp Cys Val Val Lys Phe Phe
 85 90 95

Leu Glu Thr Gly Ser Val Phe Trp Phe Phe Leu Arg Ser Glu Thr Lys
 100 105 110

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Gly	Arg	Ala	Val	Arg	His	Leu	Arg	Thr	Phe	Phe	Glu	Ala	Asn	Asn	Phe
		115					120					125			
Phe	Phe	Gly	Ser	His	Cys	Gly	Thr	Met	Glu	Tyr	Cys	Leu	Lys	Gln	Val
	130					135					140				
Leu	Thr	Glu	Thr	Glu	Ser	Ile	Ile	Asp	Ser	Phe	Cys	Glu	Glu	Arg	Asn
145					150					155					160
Arg															

and a molecular weight from about 17 to about 21 kDa, preferably about 19 kDa.

Yet another such DNA molecule (GLRaV-2 ORF8) includes nucleotides 14667-15284 of SEQ. ID. No. 1 and codes for a third undefined grapevine leafroll virus protein or polypeptide. This DNA molecule comprises a nucleotide sequence

5 corresponding to SEQ. ID. No. 18 as follows:

ATGAGGGTTA TAGTGTCTCC TTATGAAGCT GAAGACATTC TGAAAAGATC GACTGACATG	60
TTACGAAACA TAGACAGTGG GGTCTTGAGC ACTAAAGAAT GTATCAAGGC ATTCTCGACG	120
ATAACGCGAG ACCTACATTG TCGGAAGGCT TCCTACCAGT GGGGTGTTGA CACTGGGTTA	180
TATCAGCGTA ATTGCGCTGA AAAACGTTTA ATTGACACGG TGGAGTCAAA CATACGGTTG	240
GCTCAACCTC TCGTGCGTGA AAAAGTGGCG GTTCATTTTT GTAAGGATGA ACCAAAAGAG	300
CTAGTAGCAT TCATCACGCG AAAGTACGTG GAACTCACGG GCGTGGGAGT GAGAGAAGCG	360
GTGAAGAGGG AAATGCGCTC TCTTACCAAA ACAGTTTTAA ATAAATGTC TTTGGAAATG	420
GCGTTTTACA TGTCACCACG AGCGTGGAAA AACGCTGAAT GGTTAGAACT AAAATTTTCA	480
CCTGTGAAAA TCTTTAGAGA TCTGCTATTA GACGTGGAAA CGCTCAACGA ATTGTGCGCC	540
GAAGATGATG TTCACGTCGA CAAAGTAAAT GAGAATGGGG ACGAAAATCA CGACCTCGAA	600
CTCCAAGACG AATGTTAA	618

The third undefined protein or polypeptide has a deduced amino acid sequence corresponding to SEQ. ID. No. 19 as follows:

Met	Arg	Val	Ile	Val	Ser	Pro	Tyr	Glu	Ala	Glu	Asp	Ile	Leu	Lys	Arg
1				5					10					15	
Ser	Thr	Asp	Met	Leu	Arg	Asn	Ile	Asp	Ser	Gly	Val	Leu	Ser	Thr	Lys
		20						25					30		
Glu	Cys	Ile	Lys	Ala	Phe	Ser	Thr	Ile	Thr	Arg	Asp	Leu	His	Cys	Ala
	35						40					45			

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Lys Ala Ser Tyr Gln Trp Gly Val Asp Thr Gly Leu Tyr Gln Arg Asn
 50 55 60
 Cys Ala Glu Lys Arg Leu Ile Asp Thr Val Glu Ser Asn Ile Arg Leu
 65 70 75 80
 Ala Gln Pro Leu Val Arg Glu Lys Val Ala Val His Phe Cys Lys Asp
 85 90 95
 Glu Pro Lys Glu Leu Val Ala Phe Ile Thr Arg Lys Tyr Val Glu Leu
 100 105 110
 Thr Gly Val Gly Val Arg Glu Ala Val Lys Arg Glu Met Arg Ser Leu
 115 120 125
 Thr Lys Thr Val Leu Asn Lys Met Ser Leu Glu Met Ala Phe Tyr Met
 130 135 140
 Ser Pro Arg Ala Trp Lys Asn Ala Glu Trp Leu Glu Leu Lys Phe Ser
 145 150 155 160
 Pro Val Lys Ile Phe Arg Asp Leu Leu Leu Asp Val Glu Thr Leu Asn
 165 170 175
 Glu Leu Cys Ala Glu Asp Asp Val His Val Asp Lys Val Asn Glu Asn
 180 185 190
 Gly Asp Glu Asn His Asp Leu Glu Leu Gln Asp Glu Cys
 195 200 205

and a molecular weight from about 22 to about 26 kDa, preferably about 24 kDa.

Another DNA molecule of the present invention (GLRaV-2 3' UTR) includes nucleotides 15285-15500 of SEQ. ID. No. 1 and comprises a nucleotide sequence corresponding to SEQ. ID. No. 23 as follows:

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ACATTGGTTA AGTTTAACGA AAATGATTAG TAAATAATAA ATCGAACGTG GGTGTATCTA      60
CCTGACGTAT CAACTTAAGC TGTTACTGAG TAATTAAACC AACAAGTGTT GGTGTAATGT      120
GTATGTTGAT GTAGAGAAAA ATCCGTTTGT AGAACGGTGT TTTTCTCTTC TTTATTTTTA      180
AAAAAAAAAT AAAAAAAAAA AAAAAAAGC GGCCGC                                     216
  
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5 Also encompassed by the present invention are fragments of the DNA molecules of the present invention. Suitable fragments capable of imparting grapevine leafroll resistance to grape plants are constructed by using appropriate restriction sites, revealed by inspection of the DNA molecule's sequence, to: (i) insert an interposon (Felley et al., "Interposon Mutagenesis of Soil and Water Bacteria: a Family of DNA
 10 Fragments Designed for in vitro Insertion Mutagenesis of Gram-negative Bacteria," Gene, 52:147-15 (1987), which is hereby incorporated by reference) such that truncated

forms of the grapevine leafroll virus coat polypeptide or protein, that lack various amounts of the C-terminus, can be produced or (ii) delete various internal portions of the protein. Alternatively, the sequence can be used to amplify any portion of the coding region, such that it can be cloned into a vector supplying both transcription and translation start signals.

Suitable DNA molecules are those that hybridize to a DNA molecule comprising a nucleotide sequence of at least 15 continuous bases of SEQ. ID. No. 1 under stringent conditions characterized by a hybridization buffer comprising 0.9M sodium citrate ("SSC") buffer at a temperature of 37°C and remaining bound when subject to washing with SSC buffer at 37°C; and preferably in a hybridization buffer comprising 20% formamide in 0.9M saline/0.9M SSC buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2x SSC buffer at 42°C.

Variants may also (or alternatively) be modified by, for example, the deletion or addition of nucleotides that have minimal influence on the properties, secondary structure and hydropathic nature of the encoded polypeptide. For example, the nucleotides encoding a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The nucleotide sequence may also be altered so that the encoded polypeptide is conjugated to a linker or other sequence for ease of synthesis, purification, or identification of the polypeptide.

The protein or polypeptide of the present invention is preferably produced in purified form (preferably, at least about 80%, more preferably 90%, pure) by conventional techniques. Typically, the protein or polypeptide of the present invention is isolated by lysing and sonication. After washing, the lysate pellet is resuspended in buffer containing Tris-HCl. During dialysis, a precipitate forms from this protein solution. The solution is centrifuged, and the pellet is washed and resuspended in the buffer containing Tris-HCl. Proteins are resolved by electrophoresis through an SDS 12% polyacrylamide gel.

The DNA molecule encoding the grapevine leafroll virus (type 2) protein or polypeptide of the present invention can be incorporated in cells using conventional recombinant DNA technology. Generally, this involves inserting the DNA molecule into an expression system to which the DNA molecule is heterologous (i.e. not normally present). The heterologous DNA molecule is inserted into the expression system or vector in proper sense orientation and correct reading frame. The vector contains the

necessary elements for the transcription and translation of the inserted protein-coding sequences.

U.S. Patent No. 4,237,224 to Cohen and Boyer, which is hereby incorporated by reference, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including procaryotic organisms and eucaryotic cells grown in tissue culture.

Recombinant genes may also be introduced into viruses, such as vaccinia virus. Recombinant viruses can be generated by transfection of plasmids into cells infected with virus.

Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBR322, pBR325, pACYC177, pACYC184, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBluescript II SK +/- or KS +/- (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, Calif, which is hereby incorporated by reference), pQE, pIH821, pGEX, pET series (see Studier et. al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," Gene Expression Technology, vol. 185 (1990), which is hereby incorporated by reference), and any derivatives thereof. Recombinant molecules can be introduced into cells via transformation, transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Springs Laboratory, Cold Springs Harbor, New York (1982), which is hereby incorporated by reference.

A variety of host-vector systems may be utilized to express the protein-encoding sequence(s). Primarily, the vector system must be compatible with the host cell used. Host-vector systems include but are not limited to the following: bacteria transformed with bacteriophage DNA, plasmid DNA, or cosmid DNA; microorganisms such as yeast containing yeast vectors; mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); and plant cells infected by bacteria or transformed via particle bombardment (i.e. biolistics). The expression elements of these vectors vary in their

strength and specificities. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements can be used.

Different genetic signals and processing events control many levels of gene expression (e.g., DNA transcription and messenger RNA ("mRNA") translation).

5 Transcription of DNA is dependent upon the presence of a promoter which is a DNA sequence that directs the binding of RNA polymerase and thereby promotes mRNA synthesis. The DNA sequences of eucaryotic promoters differ from those of procaryotic promoters. Furthermore, eucaryotic promoters and accompanying genetic signals may not be recognized in or may not function in a procaryotic system, and,
10 further, procaryotic promoters are not recognized and do not function in eucaryotic cells.

Similarly, translation of mRNA in procaryotes depends upon the presence of the proper procaryotic signals which differ from those of eucaryotes. Efficient translation of mRNA in procaryotes requires a ribosome binding site called the Shine-Dalgarno ("SD") sequence on the mRNA. This sequence is a short nucleotide sequence
15 of mRNA that is located before the start codon, usually AUG, which encodes the amino-terminal methionine of the protein. The SD sequences are complementary to the 3'-end of the 16S rRNA (ribosomal RNA) and probably promote binding of mRNA to ribosomes by duplexing with the rRNA to allow correct positioning of the ribosome. For a review on maximizing gene expression, see Roberts and Lauer, Methods in Enzymology, 68:473
20 (1979), which is hereby incorporated by reference.

Promoters vary in their "strength" (i.e. their ability to promote transcription). For the purposes of expressing a cloned gene, it is desirable to use strong promoters in order to obtain a high level of transcription and, hence, expression of the gene. Depending upon the host cell system utilized, any one of a number of suitable
25 promoters may be used. For instance, when cloning in *E. coli*, its bacteriophages, or plasmids, promoters such as the T7 phage promoter, *lac* promoter, *trp* promoter, *recA* promoter, ribosomal RNA promoter, the P_R and P_L promoters of coliphage lambda and others, including but not limited, to *lacUV5*, *ompF*, *bla*, *lpp*, and the like, may be used to direct high levels of transcription of adjacent DNA segments. Additionally, a hybrid *trp-lacUV5* (*tac*) promoter or other *E. coli* promoters produced by recombinant DNA or other
30 synthetic DNA techniques may be used to provide for transcription of the inserted gene.

Bacterial host cell strains and expression vectors may be chosen which inhibit the action of the promoter unless specifically induced. In certain operons, the addition of specific inducers is necessary for efficient transcription of the inserted DNA.

For example, the *lac* operon is induced by the addition of lactose or IPTG (isopropylthio-beta-D-galactoside). A variety of other operons, such as *trp*, *pro*, etc., are under different controls.

Specific initiation signals are also required for efficient gene transcription and translation in procaryotic cells. These transcription and translation initiation signals may vary in "strength" as measured by the quantity of gene specific messenger RNA and protein synthesized, respectively. The DNA expression vector, which contains a promoter, may also contain any combination of various "strong" transcription and/or translation initiation signals. For instance, efficient translation in *E. coli* requires a Shine-Dalgarno ("SD") sequence about 7-9 bases 5' to the initiation codon ("ATG") to provide a ribosome binding site. Thus, any SD-ATG combination that can be utilized by host cell ribosomes may be employed. Such combinations include but are not limited to the SD-ATG combination from the *cro* gene or the *N* gene of coliphage lambda, or from the *E. coli* tryptophan E, D, C, B or A genes. Additionally, any SD-ATG combination produced by recombinant DNA or other techniques involving incorporation of synthetic nucleotides may be used.

Once the isolated DNA molecules encoding the various grapevine leafroll virus (type 2) proteins or polypeptides, as described above, have been cloned into an expression system, they are ready to be incorporated into a host cell. Such incorporation can be carried out by the various forms of transformation noted above, depending upon the vector/host cell system. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like.

The present invention also relates to RNA molecules which encode the various grapevine leafroll virus (type 2) proteins or polypeptides described above. The transcripts can be synthesized using the host cells of the present invention by any of the conventional techniques. The mRNA can be translated either *in vitro* or *in vivo*. Cell-free systems typically include wheat-germ or reticulocyte extracts. *In vivo* translation can be effected, for example, by microinjection into frog oocytes.

One aspect of the present invention involves using one or more of the above DNA molecules encoding the various proteins or polypeptides of a grapevine leafroll virus (type 2) to transform grape plants in order to impart grapevine leafroll resistance to the plants. The mechanism by which resistance is imparted is not known. In one hypothetical mechanism, the transformed plant can express a protein or polypeptide of grapevine leafroll virus (type 2), and, when the transformed plant is inoculated by a

grapevine leafroll virus, such as GLRaV-1, GLRaV-2, GLRaV-3, GLRaV-4, GLRaV-5, or GLRaV-6, or combinations of these, the expressed protein or polypeptide prevents translation of the viral DNA.

In this aspect of the present invention the subject DNA molecule incorporated in the plant can be constitutively expressed. Alternatively, expression can be regulated by a promoter which is activated by the presence of grapevine leafroll virus. Suitable promoters for these purposes include those from genes expressed in response to grapevine leafroll virus infiltration.

The isolated DNA molecules of the present invention can be utilized to impart grapevine leafroll virus resistance for a wide variety of grapevine plants. The DNA molecules are particularly well suited to imparting resistance to *Vitis* scion or rootstock cultivars. Scion cultivars which can be protected include those commonly referred to as Table or Raisin Grapes, such as Alden, Almeria, Anab-E-Shahi, Autumn Black, Beauty Seedless, Black Corinth, Black Damascus, Black Malvoisie, Black Prince, Blackrose, Bronx Seedless, Burgrave, Calmeria, Campbell Early, Canner, Cardinal, Catawba, Christmas, Concord, Dattier, Delight, Diamond, Dizmar, Duchess, Early Muscat, Emerald Seedless, Emperor, Exotic, Ferdinand de Lesseps, Fiesta, Flame seedless, Flame Tokay, Gasconade, Gold, Himrod, Hunisa, Hussiene, Isabella, Italia, July Muscat, Khandahar, Katta, Kourgane, Kishmishi, Loose Perlette, Malaga, Monukka, Muscat of Alexandria, Muscat Flame, Muscat Hamburg, New York Muscat, Niabell, Niagara, Olivette blanche, Ontario, Pierce, Queen, Red Malaga, Ribier, Rish Baba, Romulus, Ruby Seedless, Schuyler, Seneca, Suavis (IP 365), Thompson seedless, and Thomuscat. They also include those used in wine production, such as Aleatico, Alicante Bouschet, Aligote, Alvarelhao, Aramon, Baco blanc (22A), Burger, Cabernet franc, Cabernet, Sauvignon, Calzin, Carignane, Charbono, Chardonnay, Chasselas dore, Chenin blanc, Clairette blanche, Early Burgundy, Emerald Riesling, Feher Szagos, Fernao Pires, Flora, French Colombard, Fresia, Furmint, Gamay, Gewurztraminer, Grand noir, Gray Riesling, Green Hungarian, Green Veltliner, Grenache, Grillo, Helena, Inzolia, Lagrein, Lambrusco de Salamino, Malbec, Malvasia bianca, Mataro, Melon, Merlot, Meunier, Mission, Montua de Pilas, Muscadelle du Bordelais, Muscat blanc, Muscat Ottonel, Muscat Saint-Vallier, Nebbiolo, Nebbiolo fino, Nebbiolo Lampia, Orange Muscat, Palomino, Pedro Ximenes, Petit Bouschet, Petite Sirah, Peverella, Pinot noir, Pinot Saint-George, Primitivo di Gioia, Red Veltliner, Refosco, Rkatsiteli, Royalty, Rubired, Ruby Cabernet, Saint-Emilion, Saint Macaire, Salvador, Sangiovese, Sauvignon blanc,

Sauvignon gris, Sauvignon vert, Scarlet, Seibel 5279, Seibel 9110, Seibel 13053, Semillon, Servant, Shiraz, Souzao, Sultana Crimson, Sylvaner, Tannat, Teroldico, Tinta Madeira, Tinto cao, Touriga, Traminer, Trebbiano Toscano, Trousseau, Valdepenas, Viognier, Walschriesling, White Riesling, and Zinfandel. Rootstock cultivars which can be protected include Couderc 1202, Couderc 1613, Couderc 1616, Couderc 3309, Dog Ridge, Foex 33 EM, Freedom, Ganzin 1 (A x R #1), Harmony, Kober 5BB, LN33, Millardet & de Grasset 41B, Millardet & de Grasset 420A, Millardet & de Grasset 101-14, Oppenheim 4 (SO4), Paulsen 775, Paulsen 1045, Paulsen 1103, Richter 99, Richter 110, Riparia Gloire, Ruggeri 225, Saint-George, Salt Creek, Teleki 5A, *Vitis rupestris* Constantia, *Vitis californica*, and *Vitis girdiana*.

There exists an extensive similarity in the hsp70-related sequence regions of GLRaV-2 and other closteroviruses, such as tristeza virus and beet yellows virus. Consequently, the GLRaV-2 hsp70-related gene can also be used to produce transgenic plants or cultivars other than grape, such as citrus or sugar beet, which are resistant to closteroviruses other than grapevine leafroll, such as tristeza virus and beet yellows virus.

Suitable citrus cultivars include lemon, lime, orange, grapefruit, pineapple, tangerine, and the like, such as Joppa, Maltaise Ovale, Parson (Parson Brown), Pera, Pineapple, Queen, Shamouti, Valencia, Tenerife, Imperial Doblefina, Washington Sanguine, Moro, Sanguinello Moscato, Spanish Sanguinelli, Tarocco, Atwood, Australian, Bahia, Baiana, Cram, Dalmau, Eddy, Fisher, Frost Washington, Gillette, LengNavelina, Washington, Satsuma Mandarin, Dancy, Robinson, Ponkan, Duncan, Marsh, Pink Marsh, Ruby Red, Red Seedless, Smooth Seville, Orlando Tangelo, Eureka, Lisbon, Meyer Lemon, Rough Lemon, Sour Orange, Persian Lime, West Indian Lime, Bearss, Sweet Lime, Troyer Citrange, and Citrus Trifoliata. Each of these citrus cultivars is suitable for producing transgenic citrus plants resistant to tristeza virus.

The economically important species of sugar beet is *Beta vulgaris* L., which has four important cultivar types: sugar beet, table beet, fodder beet, and Swiss chard. Each of these beet cultivars is suitable for producing transgenic beet plants resistant to beet yellows virus, as described above.

Because GLRaV-2 has been known to infect tobacco plants (e.g., *Nicotiana benthamiana*), it is also desirable to produce transgenic tobacco plants which are resistant to grapevine leafroll viruses, such as GLRaV-2.

Plant tissue suitable for transformation include leaf tissue, root tissue, meristems, zygotic and somatic embryos, and anthers. It is particularly preferred to utilize embryos obtained from anther cultures.

The expression system of the present invention can be used to transform
5 virtually any plant tissue under suitable conditions. Tissue cells transformed in accordance with the present invention can be grown *in vitro* in a suitable medium to impart grapevine leafroll virus resistance. Transformed cells can be regenerated into whole plants such that the protein or polypeptide imparts resistance to grapevine leafroll virus in the intact transgenic plants. In either case, the plant cells transformed with the recombinant DNA expression
10 system of the present invention are grown and caused to express that DNA molecule to produce one of the above-described grapevine leafroll virus proteins or polypeptides and, thus, to impart grapevine leafroll virus resistance.

In producing transgenic plants, the DNA construct in a vector described above can be microinjected directly into plant cells by use of micropipettes to transfer mechanically
15 the recombinant DNA. Crossway, Mol. Gen. Genetics, 202:179-85 (1985), which is hereby incorporated by reference. The genetic material may also be transferred into the plant cell using polyethylene glycol. Krens, et al., Nature, 296:72-74 (1982), which is hereby incorporated by reference.

One technique of transforming plants with the DNA molecules in
20 accordance with the present invention is by contacting the tissue of such plants with an inoculum of a bacteria transformed with a vector comprising a gene in accordance with the present invention which imparts grapevine leafroll resistance. Generally, this procedure involves inoculating the plant tissue with a suspension of bacteria and incubating the tissue for 48 to 72 hours on regeneration medium without antibiotics at 25-
25 28°C.

Bacteria from the genus *Agrobacterium* can be utilized to transform plant cells. Suitable species of such bacterium include *Agrobacterium tumefaciens* and *Agrobacterium rhizogenes*. *Agrobacterium tumefaciens* (e.g., strains C58, LBA4404, or EHA105) is particularly useful due to its well-known ability to transform plants.

30 Heterologous genetic sequences can be introduced into appropriate plant cells, by means of the Ti plasmid of *A. tumefaciens* or the Ri plasmid of *A. rhizogenes*. The Ti or Ri plasmid is transmitted to plant cells on infection by *Agrobacterium* and is stably integrated into the plant genome. J. Schell, Science, 237:1176-83 (1987), which is hereby incorporated by reference.

After transformation, the transformed plant cells must be regenerated.

Plant regeneration from cultured protoplasts is described in Evans et al., Handbook of Plant Cell Cultures, Vol. 1: (MacMillan Publishing Co., New York, 1983); and Vasil I.R. (ed.), Cell Culture and Somatic Cell Genetics of Plants, Acad. Press, Orlando, Vol. I, 1984, and Vol. III (1986), which are hereby incorporated by reference.

It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to, all major species of sugarcane, sugar beets, cotton, fruit trees, and legumes.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

After the expression cassette is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

Once transgenic plants of this type are produced, the plants themselves can be cultivated in accordance with conventional procedure so that the DNA construct is present in the resulting plants. Alternatively, transgenic seeds are recovered from the transgenic plants. These seeds can then be planted in the soil and cultivated using conventional procedures to produce transgenic plants.

Another approach to transforming plant cells with a gene which imparts resistance to pathogens is particle bombardment (also known as biolistic transformation) of the host cell. This can be accomplished in one of several ways. The first involves propelling inert or biologically active particles at cells. This technique is disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792, all to Sanford et al., and in Emerschad et al., "Somatic Embryogenesis and Plant Development from Immature Zygotic Embryos of Seedless Grapes (*Vitis vinifera*)," Plant Cell Reports, 14:6-12 (1995) ("Emerschad (1995)"), which are hereby incorporated by reference. Generally, this procedure involves propelling inert or biologically active particles at the cells under

conditions effective to penetrate the outer surface of the cell and to be incorporated within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the heterologous DNA.

Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells.

Once a grape plant tissue, citrus plant tissue, beet plant tissue, or tobacco plant tissue is transformed in accordance with the present invention, the transformed tissue is regenerated to form a transgenic plant. Generally, regeneration is accomplished by culturing transformed tissue on medium containing the appropriate growth regulators and nutrients to allow for the initiation of shoot meristems. Appropriate antibiotics are added to the regeneration medium to inhibit the growth of *Agrobacterium* and to select for the development of transformed cells. Following shoot initiation, shoots are allowed to develop tissue culture and are screened for marker gene activity.

The DNA molecules of the present invention can be made capable of transcription to a messenger RNA, which, although encoding for a grapevine leafroll virus (type 2) protein or polypeptide, does not translate to the protein. This is known as RNA-mediated resistance. When a *Vitis* scion or rootstock cultivar, or a citrus, beet, or tobacco cultivar, is transformed with such a DNA molecule, the DNA molecule can be transcribed under conditions effective to maintain the messenger RNA in the plant cell at low level density readings. Density readings of between 15 and 50 using a Hewlett ScanJet and Image Analysis Program are preferred.

A portion of one or more DNA molecules of the present invention as well as other DNA molecules can be used in a transgenic grape plant, citrus plant, beet plant, or tobacco plant in accordance with U.S. Patent Application Serial No. 09/025,635, which is hereby incorporated herein by reference.

The grapevine leafroll virus (type 2) protein or polypeptide of the present invention can also be used to raise antibodies or binding portions thereof or probes. The antibodies can be monoclonal or polyclonal.

Monoclonal antibody production may be effected by techniques which are well-known in the art. Basically, the process involves first obtaining immune cells (lymphocytes) from the spleen of a mammal (e.g., mouse) which has been previously immunized with the antigen of interest either *in vivo* or *in vitro*. The antibody-secreting lymphocytes are then fused with (mouse) myeloma cells or transformed cells, which are

capable of replicating indefinitely in cell culture, thereby producing an immortal, immunoglobulin-secreting cell line. The resulting fused cells, or hybridomas, are cultured, and the resulting colonies screened for the production of the desired monoclonal antibodies. Colonies producing such antibodies are cloned, and grown either *in vivo* or *in vitro* to produce large quantities of antibody. A description of the theoretical basis and practical methodology of fusing such cells is set forth in Kohler and Milstein, Nature, 256:495 (1975), which is hereby incorporated by reference.

Mammalian lymphocytes are immunized by *in vivo* immunization of the animal (e.g., a mouse) with the protein or polypeptide of the present invention. Such immunizations are repeated as necessary at intervals of up to several weeks to obtain a sufficient titer of antibodies. Following the last antigen boost, the animals are sacrificed and spleen cells removed.

Fusion with mammalian myeloma cells or other fusion partners capable of replicating indefinitely in cell culture is effected by standard and well-known techniques, for example, by using polyethylene glycol ("PEG") or other fusing agents. (See Milstein and Kohler, Eur. J. Immunol., 6:511 (1976), which is hereby incorporated by reference.) This immortal cell line, which is preferably murine, but may also be derived from cells of other mammalian species, including but not limited to rats and humans, is selected to be deficient in enzymes necessary for the utilization of certain nutrients, to be capable of rapid growth, and to have good fusion capability. Many such cell lines are known to those skilled in the art, and others are regularly described.

Procedures for raising polyclonal antibodies are also well known. Typically, such antibodies can be raised by administering the protein or polypeptide of the present invention subcutaneously to New Zealand white rabbits which have first been bled to obtain pre-immune serum. The antigens can be injected at a total volume of 100 µl per site at six different sites. Each injected material will contain synthetic surfactant adjuvant pluronic polyols, or pulverized acrylamide gel containing the protein or polypeptide after SDS-polyacrylamide gel electrophoresis. The rabbits are then bled two weeks after the first injection and periodically boosted with the same antigen three times every six weeks. A sample of serum is then collected 10 days after each boost. Polyclonal antibodies are then recovered from the serum by affinity chromatography using the corresponding antigen to capture the antibody. Ultimately, the rabbits are euthenized with pentobarbital 150 mg/Kg IV. This and other procedures for raising

polyclonal antibodies are disclosed in Harlow et. al., editors, Antibodies: A Laboratory Manual (1988), which is hereby incorporated by reference.

In addition to utilizing whole antibodies, binding portions of such antibodies can be used. Such binding portions include Fab fragments, F(ab')₂ fragments, and Fv fragments. These antibody fragments can be made by conventional procedures, such as proteolytic fragmentation procedures, as described in Goding, Monoclonal Antibodies: Principles and Practice, New York:Academic Press, pp. 98-118 (1983), which is hereby incorporated by reference.

The present invention also relates to probes found either in nature or prepared synthetically by recombinant DNA procedures or other biological procedures. Suitable probes are molecules which bind to grapevine leafroll (type 2) viral antigens identified by the monoclonal antibodies of the present invention. Such probes can be, for example, proteins, peptides, lectins, or nucleic acid probes.

The antibodies or binding portions thereof or probes can be administered to grapevine leafroll virus infected scion cultivars or rootstock cultivars. Alternatively, at least the binding portions of these antibodies can be sequenced, and the encoding DNA synthesized. The encoding DNA molecule can be used to transform plants together with a promoter which causes expression of the encoded antibody when the plant is infected by grapevine leafroll virus. In either case, the antibody or binding portion thereof or probe will bind to the virus and help prevent the usual leafroll response.

Antibodies raised against the GLRaV-2 proteins or polypeptides of the present invention or binding portions of these antibodies can be utilized in a method for detection of grapevine leafroll virus in a sample of tissue, such as tissue (e.g., scion or rootstock) from a grape plant or tobacco plant. Antibodies or binding portions thereof suitable for use in the detection method include those raised against a helicase, a methyltransferase, a papain-like protease, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a coat protein, a diverged coat protein, or other proteins or polypeptides in accordance with the present invention. Any reaction of the sample with the antibody is detected using an assay system which indicates the presence of grapevine leafroll virus in the sample. A variety of assay systems can be employed, such as enzyme-linked immunosorbent assays, radioimmunoassays, gel diffusion precipitin reaction assays, immunodiffusion assays, agglutination assays, fluorescent immunoassays, protein A immunoassays, or immunoelectrophoresis assays.

Alternatively, grapevine leafroll virus can be detected in such a sample using a nucleotide sequence of the DNA molecule, or a fragment thereof, encoding for a protein or polypeptide of the present invention. The nucleotide sequence is provided as a probe in a nucleic acid hybridization assay or a gene amplification detection procedure (e.g., using a polymerase chain reaction procedure). The nucleic acid probes of the present invention may be used in any nucleic acid hybridization assay system known in the art, including, but not limited to, Southern blots (Southern, E.M., "Detection of Specific Sequences Among DNA Fragments Separated by Gel Electrophoresis," J. Mol. Biol., 98:503-17 (1975), which is hereby incorporated by reference), Northern blots (Thomas, P.S., "Hybridization of Denatured RNA and Small DNA Fragments Transferred to Nitrocellulose," Proc. Nat'l Acad. Sci. USA, 77:5201-05 (1980), which is hereby incorporated by reference), and Colony blots (Grunstein, M., et al., "Colony Hybridization: A Method for the Isolation of Cloned cDNAs that Contain a Specific Gene," Proc. Nat'l Acad. Sci. USA, 72:3961-65 (1975), which is hereby incorporated by reference). Alternatively, the probes can be used in a gene amplification detection procedure (e.g., a polymerase chain reaction). Erlich, H.A., et. al., "Recent Advances in the Polymerase Chain Reaction," Science 252:1643-51 (1991), which is hereby incorporated by reference. Any reaction with the probe is detected so that the presence of a grapevine leafroll virus in the sample is indicated. Such detection is facilitated by providing the probe of the present invention with a label. Suitable labels include a radioactive compound, a fluorescent compound, a chemiluminescent compound, an enzymatic compound, or other equivalent nucleic acid labels.

Depending upon the desired scope of detection, it is possible to utilize probes having nucleotide sequences that correspond with conserved or variable regions of the ORF or UTR. For example, to distinguish a grapevine leafroll virus from other related viruses (e.g., other closteroviruses), it is desirable to use probes which contain nucleotide sequences that correspond to sequences more highly conserved among all grapevine leafroll viruses. Also, to distinguish between different grapevine leafroll viruses (i.e., GLRaV-2 from GLRaV-1, GLRaV-3, GLRaV-4, GLRaV-5, and GLRaV-6), it is desirable to utilize probes containing nucleotide sequences that correspond to sequences less highly conserved among the different grapevine leafroll viruses.

Nucleic acid (DNA or RNA) probes of the present invention will hybridize to complementary GLRaV-2 nucleic acid under stringent conditions. Generally, stringent conditions are selected to be about 50°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under

defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. The T_m is dependent upon the solution conditions and the base composition of the probe, and may be calculated using the following equation:

$$\begin{aligned} T_m = 79.8^{\circ}\text{C} &+ (18.5 \times \text{Log}[\text{Na}^+]) \\ &+ (58.4^{\circ}\text{C} \times \%[\text{G}+\text{C}]) \\ &- (820 / \# \text{bp in duplex}) \\ &- (0.5 \times \% \text{ formamide}) \end{aligned}$$

Nonspecific binding may also be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein-containing solutions, addition of heterologous RNA, DNA, and SDS to the hybridization buffer, and treatment with RNase. Wash conditions are typically performed at or below stringency. Generally, suitable stringent conditions for nucleic acid hybridization assays or gene amplification detection procedures are as set forth above. More or less stringent conditions may also be selected.

EXAMPLES

The following examples are provided to illustrate embodiments of the present invention but are by no means intended to limit its scope.

Example 1 - Northern Hybridization

Specificity of the selected clones was confirmed by Northern hybridization. Northern hybridization was performed after electrophoresis of the dsRNA of GLRaV-2 in 1% agarose non-denaturing condition gel. The agarose gel was denatured by soaking in 50 mM NaOH containing 0.4 M NaCl for 30 min, and then neutralized with 0.1 M Tris-HCl (PH7.5) containing 0.5 M NaCl for another 30 min. RNA was sandwich blotted overnight onto Genescreen™ plus membrane (Dupont NEN Research Product) in 10 X SSC buffer and hybridized as described by the manufacturer's instructions (DuPont, NEN).

Example 2 - Sequencing and Computer Assisted Nucleotide and Amino Acid Sequence Analysis

DNA inserts were sequenced in pBluescript SK+ by using T3 and T7 universal primers for the terminal region sequence and additional oligonucleotide primers

designed according to the known sequence for the internal region sequence. Purification of plasmid DNA was performed by a modified mini alkaline-lysis/PEG precipitation procedure described by the manufacturer (Applied Biosystems, Inc.). Nucleotide sequencing was performed on both strands of cDNA by using ABI TaqDyeDeoxy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc.). Automatic sequencing was performed on an ABI373 Automated Sequencer (Applied Biosystems, Inc.) at Cornell University, Geneva, NY.

The nucleotide sequences of GLRaV-2 were assembled and analyzed with the programs of EditSeq and SeqMan, respectively, of DNASTAR package (Madison, WI).

Amino acid sequences deduced from nucleotide sequences and its encoding open reading frames were conducted using the MapDraw program. Multiple alignments of amino acid sequences, identification of consensus amino acid sequences, and generation of phylogenetic trees were performed using the Clustal method in the MegAlign program. The nucleotide and amino acid sequences of other closteroviruses were obtained with the Entrez Program; and sequence comparisons with nonredundant databases were searched with the Blast Program from the National Center for Biotechnology Information.

Example 3 - Isolation of dsRNA

Several vines of GLRaV-2 infected *Vitis vinifera* cv Pinot Noir that originated from a central New York vineyard served as the source for dsRNA isolation and cDNA cloning. dsRNA was extracted from phloem tissue of infected grapevines according to the method described by Hu et al., "Characterization of Closterovirus-Like Particles Associated with Grapevine Leafroll Disease," J. Phytopathology 128:1-14 (1990), which is hereby incorporated by reference. Purification of the high molecular weight dsRNA (ca 15 kb) was carried out by electrophoretic separation of the total dsRNA on a 0.7% low melting point agarose gel and extraction by phenol/chloroform following the method described by Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, New York (1989), which is hereby incorporated by reference. Concentration of dsRNA was estimated with UV fluorescent density of an ethidium bromide stained dsRNA band in comparison with a known concentration of DNA marker.

Example 4 - cDNA Synthesis and Cloning

cDNA synthesis was performed following the method initially described by Jelkmann et al., "Cloning of Four Plant Viruses From Small Quantities of Double-Stranded RNA," *Phytopathology* 79:1250-53 (1989) and modified by Ling et al., "The Coat Protein Gene of Grapevine Leafroll Associated Closterovirus-3: Cloning, Nucleotide Sequencing and Expression in Transgenic Plants," *Arch. Virology* 142:1101-16 (1997), both of which are hereby incorporated by reference. About 100 ng of high molecular weight dsRNA purified from low melting agarose gel was denatured in 20 mM methylmercuric hydroxide and incubated at room temperature for 10 min with 350 ng of random primers. First strand cDNA was synthesized by using avian myeloblastosis virus (AMV) reverse transcriptase. Second strand cDNA was obtained by using RNase H and *E.coli* DNA polymerase I. Double-stranded cDNA was blunt ended with T4 DNA polymerase and ligated with EcoR I adapters. The cDNA, which had EcoR I adapters at the ends, was activated by kinase reaction and ligated into Lambda ZAP II/EcoR I prepared arms following the manufacturer's instruction (Stratagene). The recombinant DNA was then packaged *in vitro* to Gigapack[®] II packaging extract (Stratagene). The packaged phage particles were amplified and titered according to the manufacturer's instruction.

Two kinds of probes were used to identify GLRaV-2 specific clones from the library. One type was prepared from the synthesized cDNA that was amplified by PCR after ligation to the specific EcoR I Uni-Amp[™] adapters (Clontech); and the other type was DNA inserts or PCR products from already sequenced clones. Clones from the cDNA library were selected by colony-lifting hybridization onto the colony/plaque Screen membrane (NEN Research Product) with the probe described above. The probe was prepared by labeling with ³²P [α -dATP] using Klenow fragment of *E.coli* DNA polymerase I. Prehybridization, hybridization, and washing steps were carried out at 65°C according to the manufacturer's instruction (Dupont, NEN Research Product). Selected plaques were converted to recombinant pBluescript by *in vivo* excision method according to the manufacturer's instruction (Stratagene).

To obtain clones representing the extreme 3'-terminus of GLRaV-2, dsRNA was polyadenylated by yeast poly(A) polymerase. Using poly(A)-tailed dsRNA as template, cDNA was amplified by RT-PCR with oligo(dT)18 and a specific primer, CP-1/T7R, which

is derived from the clone CP-1 and has a nucleotide sequence according to SEQ. ID. No. 20 as follows:

TGCTGGAGCT TGAGGTTCTG C

21

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The resulting PCR product (3'-PCR) was cloned into a TA vector (Invitrogen) and sequenced.

10

As shown in Figure 1A, a high molecular weight dsRNA of ca. 15 kb was consistently identified from GLRaV-2 infected grapevines, but not from healthy vines. In addition, several low molecular weight dsRNAs were also detected from infected tissue. The yield of dsRNA of GLRaV-2 was estimated between 5-10 ng/15 g phloem tissue, which was much lower than that of GLRaV-3 (Hu et al., "Characterization of Closterovirus-Like Particles Associated with Grapevine Leafroll Disease," *J. Phytopathology* 128:1-14 (1990), which is hereby incorporated by reference). Only the high molecular weight dsRNA that was purified from low melting point agarose gel was used for cDNA synthesis, cloning and establishment of the Lambda/ZAP II cDNA library.

15

Two kinds of probes were used for screening the cDNA library. The initial clones were identified by hybridization with Uni-Amp™ PCR-amplified cDNA as probes. The specificity of these clones (e.g., TC-1) ranging from 200 to 1,800 bp in size was confirmed by Northern hybridization to dsRNA of GLRaV-2 as shown in Figure 1B. Additionally, over 40 different clones ranging from 800 to 7,500 bp in size were identified following hybridization with the probes generated from GLRaV-2 specific cDNA clones or from PCR products. Over 40 clones were then sequenced on the both strands (Figure 2).

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25 **Example 5 - Expression of the Coat Protein in *E. coli* and Immunoblotting**

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To determine that ORF6 was the coat protein gene of GLRaV-2, the complete ORF6 DNA molecule was subcloned from a PCR product and inserted into the fusion protein expression vector pMAL-C2 (New England Biolabs, Inc.). The specific primers used for the PCR reaction were CP-96F and CP-96R, in which an EcoR I or BamH I site was included to facilitate cloning. CP-96F was designed to include the start codon of the CP and comprises a nucleotide sequence according to SEQ. ID. NO. 21 as follows:

CGGAATTCAC CATGGAGTTG ATGTCCGACA G

31

CP-96R was 66 nucleotides downstream of the stop codon of the CP and comprises the nucleotide sequence corresponding to SEQ. ID. No. 22 as follows:

AGCGGATCCA TGGCAGATTC GTGCGTAGCA GTA

33

The coat protein was expressed as a fusion protein with maltose binding protein (MBP) of *E. coli* under the control of a “tac” promoter and suppressed by the “lac” repressor. The MBP-CP fusion protein was induced by adding 0.3 mM isopropyl- β -D-thio-gloactopyranoside (IPTG) and purified by a one step affinity column according to the manufacturer’s instruction (New England, Biolabs, Inc). The MBP-CP fusion protein or the coat protein cleaved from the fusion protein was tested to react with specific antiserum of GLRaV-2 (kindly provided by Dr. Charles Greif of INRA, Colmar, France) on Western blot according to the method described by Hu et al., “Characterization of Closterovirus-Like Particles Associated with Grapevine Leafroll Disease,” *J. Phytopathology* 128:1-14 (1990), which is hereby incorporated by reference. In contrast, the non-recombinant plasmids or uninduced cells did not react to the antiserum of GLRaV-2.

Example 6 - Sequence Analysis and Genome Organization of GLRaV-2

A total of 15,500 bp of the RNA genome of GLRaV-2 was sequenced and deposited in GenBank (accession number AF039204). About 85% of the total RNA genome was revealed from at least two different clones. The sequence in the coat protein gene region was determined and confirmed from several different overlapping clones. The genome organization of GLRaV-2, shown in Figure 2, includes nine open reading frames (e.g., ORF1a, 1b-8).

ORF1a and ORF1b: Analysis of the amino acid sequence of the N-terminal portion of GLRaV-2 ORF1a encoded product revealed two putative papain-like protease domains, which showed significant similarity to the papain-like leader protease of BYV (Agranovsky et al., “Beet Yellowings Closterovirus: Complete Genome Structure and Identification of a Papain-like Thiol Protease,” *Virology* 198:311-24 (1994), which is hereby incorporated by reference). Thus, it allowed prediction of the catalytic cysteine and histidine residues for the putative GLRaV-2 protease. Upon alignment of the sequence of the papain-like protease of BYV with that of GLRaV-2, the cleavage site at residues Gly-Gly (amino acid 588-589) of BYV aligned with the corresponding alanine-glycine (Ala-Gly) and Gly-Gly dipeptide of GLRaV-2 (Figure 3A). Cleavage at this site would result in a leader protein and

a 234 kDa (2090 amino acid) C-terminal fragment consisting of MT and HEL domains. However, the region upstream of the papain-like protease domain in GLRaV-2 did not show similarity to the corresponding region of BYV. In addition, variability in the residues located at the scissible bond (Gly in the BYV and Ala in the GLRaV-2) was present. Similar
5 variability of the cleavage site residue in the P-PRO domain has been described in LChV (Jelkmann et al., "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus. J. General Virology 78:2067-71 (1997), which is hereby incorporated by reference).

Database searching with the deduced amino acid sequence of the ORF1a/1b
10 encoded protein revealed a significant similarity to the MT, HEL and RdRP domains of the other closteroviruses. The region downstream of the P-PRO cleavage site showed a significant similarity (57.4% identity in a 266-residues alignment) to the putative methyltransferase domain of BYV and contained all the conserved motifs typical of positive-strand RNA viral type I MTs (Figure 3B). The C-terminal portion of the ORF1a was
15 identified as a helicase domain, the sequence of which showed a high similarity (57.1% identity in a 315-residues alignment) to the helicase domain of BYV and contained the seven conserved motifs characteristic of the Superfamily I helicase of positive-strand RNA viruses (Figure 3C) (Hodgman, "A New Superfamily of Replicative Proteins," Nature 333:22-23 (1988); Koonin and Dolja, "Evolution and Taxonomy of Positive-strand RNA Viruses:
20 Implications of Comparative Analysis of Amino Acid Sequences," Crit. Rev. in Biochem. and Mol. Biol. 28:375-430 (1993), both of which are hereby incorporated by reference).

ORF1b encoded a 460 amino acid polypeptide with a molecular mass of 52,486 Da, counting from the frameshifting site. Database searching with the RdRP showed a significant similarity to the RdRP domains of positive strand RNA viruses. Comparison of
25 the RdRP domains of GLRaV-2 and BYV showed the presence of the eight conserved motifs of RdRP (Figure 3D).

As shown in Figure 8, a tentative phylogenetic tree of the RdRP of GLRaV-2 with respect to other closteroviruses shows that it is closely related to the monopartite closteroviruses BYV, BYSV, and CTV.

30 In closteroviruses, a +1 ribosomal frameshift mechanism has been suggested to be involved in the expression of ORF1b as a large fusion protein with ORF1a (Agranovsky et al., "Beet Yellows Closterovirus: Complete Genome Structure and Identification of a Papain-like Thiol Protease," Virology 198:311-24 (1994); Karasev et al., "Complete Sequence of the Citrus Tristeza Virus RNA Genome," Virology 208:511-20 (1995); Klaassen

et al., "Genome Structure and Phylogenetic Analysis of Lettuce Infectious Yellow Virus, a Whitefly-Transmitted, Bipartite Closterovirus," Virology 208:99-110 (1995); Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses," Virology 221:199-207 (1996); Jelkmann et al.,

5 "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus," J. General Virology 78:2067-71 (1997), all of which are hereby incorporated by reference). In the overlapping ORF1a/1b region of BYV, the slippery sequence of GGGUUA and two hairpins structure (stem-loop and pseudoknot) are believed to result in a +1 frameshift (Agranovsky et al., "Beet Yellow Virus Closterovirus: Complete

10 Genome Structure and Identification of a Papain-like Thiol Protease," Virology 198:311-24 (1994), which is hereby incorporated by reference). None of these features are conserved in CTV and BYSV (Karasev et al., "Complete Sequence of the Citrus Tristeza Virus RNA Genome," Virology 208:511-20 (1995); Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses,"

15 Virology 221:199-207 (1996), both of which are hereby incorporated by reference), in which a ribosomal pausing at a terminator or at a rare codon was suggested to perform the same function. Comparisons of the nucleotide sequence of the C-terminal region of the helicase and the N-terminal region of RdRP of GLRaV-2 with the same region of other closteroviruses revealed a significant similarity to BYV, BYSV, and CTV. As shown in

20 Figure 4, the terminator UAG at the end of C'-terminal helicase of GLRaV-2 aligned with the terminator UAG of BYV and BYSV, and arginine CGG codon of CTV.

ORF2 encodes a small protein consisting of 171 bp (57 amino acid) with a molecular mass of 6,297 Da. As predicted, the deduced amino acid sequence includes a stretch of nonpolar amino acids, which is presumed to form a transmembrane helix. A small

25 hydrophobic analogous protein is also present in BYV, BYSV, CTV, LIYV, and LChV (Agranovsky et al. "Nucleotide Sequence of the 3'-Terminal Half of Beet Yellow Virus Closterovirus RNA Genome Unique Arrangement of Eight Virus Genes," J. General Virology 72:15-24 (1991); Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses," Virology

30 221:199-207 (1996); Pappu et al., "Nucleotide Sequence and Organization of Eight 3' Open Reading Frames of the Citrus Tristeza Closterovirus Genome," Virology 199:35-46 (1994); Klaassen et al., "Partial Characterization of the Lettuce Infectious Yellow Virus Genomic RNAs, Identification of the Coat Protein Gene and Comparison of its Amino Acid Sequence With Those of Other Filamentous RNA Plant Viruses," J. General Virology 75:1525-33

(1994); Jelkmann et al., "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus," J. General Virology 78:2067-71 (1997), all of which are hereby incorporated by reference).

ORF3 encodes a 600 amino acid polypeptide with a molecular mass of 65,111

- 5 Da, which is homologous to the HSP70 cellular heat shock protein. HSP70 is highly conserved among closteroviruses and is probably involved in ATPase activity and the protein to protein interaction for chaperone activity (Agranovsky et al. "The Beet Yellows Closterovirus p65 Homologue of HSP70 Chaperones has ATPase Activity Associated with its Conserved N-terminal Domain but Interact with Unfolded Protein Chains," J. General Virology 78:535-42 (1997); Agranovsky et al., "Bacterial Expression and Some Properties of the p65, a Homologue of Cell Heat Shock Protein HSP70 Encoded in RNA Genome of Beet Yellows Closterovirus," Doklady Akademii Nauk, 340:416-18 (1995); Karasev et al., "HSP70-Related 65-kDa Protein of Beet Yellows Closterovirus is a Microtubule-Binding Protein," FEBS Letters 304:12-14 (1992), all of which are hereby incorporated by reference).
- 10 As shown in Figure 5, alignment of the complete ORF3 of GLRaV-2 with HSP70 homolog of BYV revealed the presence of the eight conserved motifs. The percentage similarity of the HSP70 between GLRaV-2 and that of BYV, BYSV, CTV, LIYV, and LChV is 47.8%, 47.2%, 38.6%, 20.9%, and 17.7%, respectively.

ORF4 encodes a 551 amino acid protein with a molecular mass of 63,349 Da.

- 20 Database searching with the ORF4 protein product did not identify similar proteins except those of its counterparts in closteroviruses, BYV (P64), BYSV (P61), CTV (P61), LIYV (P59), and LChV (P61). This protein is believed to be a putative heat shock 90 protein. As shown in Figure 9, two conserved motifs which were present in BYV (Agranovsky et al. "Nucleotide Sequence of the 3'-Terminal Half of Beet Yellows Closterovirus RNA Genome Unique Arrangement of Eight Virus Genes," J. General Virology 72:15-24 (1991), which is hereby incorporated by reference) and CTV (Pappu et al., "Nucleotide Sequence and Organization of Eight 3' Open Reading Frames of the Citrus Tristeza Closterovirus Genome," Virology 199:35-46 (1994), which is hereby incorporated by reference) were also identified in the ORF4 of GLRaV-2.

- 30 ORF5 and ORF6 encode polypeptides with molecular mass of 24,803 Da and 21,661 Da, respectively. The start codon for both ORFs is in a favorable context for translation. ORF6 was identified as the coat protein gene of GLRaV-2 based on the sequence comparison with other closteroviruses. The calculated molecular mass of the protein product of ORF6 (21,662 Da) is in good agreement with the previously estimated 22~26 kDa based

on SDS-PAGE (Zimmermann et al., "Characterization and Serological Detection of Four Closterovirus-like Particles Associated with Leafroll Disease on Grapevine," J. Phytopathology 130:205-18 (1990); Boscia et al., "Nomenclature of Grapevine Leafroll-Associated Putative Closteroviruses," Vitis 34:171-75 (1995), both of which are hereby
5 incorporated by reference).

Database searching with the deduced amino acid sequence of the ORF6 of GLRaV-2 showed a similarity with the coat proteins of closteroviruses, BYV, BYSV, CTV, LIYV, LChV, and GLRaV-3. At the nucleotide level, the highest percentage similarity was with the coat protein of BYSV (34.8%); at the amino acid level, the highest percentage
10 similarity was with the coat proteins of BYV (32.7%) and BYSV (32.7%). As shown in Figure 6A, alignment of the amino acid sequence of the coat protein and coat protein duplicate of GLRaV-2 with respect to other closteroviruses revealed that the invariant amino acid residues (N. R. G. D.) were present in both ORF5 and ORF6 of GLRaV-2. Two of these amino acid residues (R and D) are believed to be involved in stabilization of molecules
15 by salt bridge formation and proper folding in the most conserved core region of coat proteins of all filamentous plant viruses (Dolja et al., "Phylogeny of Capsid Proteins of Rod-Shaped and Filamentous RNA Plant Viruses Two Families With Distinct Patterns of Sequence and Probably Structure Conservation," Virology 184:79-86 (1991), which is hereby incorporated by reference).

Identification of ORF6 as the coat protein gene was further confirmed by Western blot following expression of a fusion protein, consisting of a 22 kDa of ORF6 CP and a 42 kDa of maltose binding protein, produced by transformed *E. coli* as described in Example 5 *supra*. As shown in Figure 6B, the putative phylogenetic tree of the coat protein and coat protein duplicate of GLRaV-2 with those of other closteroviruses showed that
20 GLRaV-2 is more closely related to aphid transmissible closteroviruses (BYV, BYSV, and CTV) (Candresse, "Closteroviruses and Closterovirus-like Elongated Plant Viruses," in Encyclopedia of Virology, pp. 242-48, Webster and Granoff, eds., Academic Press, New York (1994), which is hereby incorporated by reference) than to whitefly (LIYV) or mealybug transmissible closteroviruses (LChV and GLRaV-3) (Raine et al., "Transmission
25 of the Agent Causing Little Cherry Disease by the Apple Mealybug *Phenacoccus aceris* and the Dodder *Cuscuta Lupuliformis*," Canadian J. Plant Pathology 8:6-11 (1986); Jelkmann et al., "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus," J. General Virology 78:2067-71 (1997); Rosciglione and Gugerli, "Transmission of Grapevine Leafroll Disease and an Associated Closterovirus
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to Healthy Grapevine by the Mealybug *Planococcus ficus*," *Phytoparasitica* 17:63 (1989); Engelbrecht and Kasdorf, "Transmission of Grapevine Leafroll Disease and Associated Closteroviruses by the Vine Mealybug *planococcus-ficus*," *Phytophactica*, 22:341-46 (1990); Cabaleiro and Segura, 1997; Petersen and Charles, "Transmission of Grapevine

5 Leafroll-Associated Closteroviruses by *Pseudococcus longispinus* and *P. calceolariae*. *Plant Pathology* 46:509-15 (1997), all of which are hereby incorporated by reference).

ORF7 and ORF8 encode polypeptides of 162 amino acid with a molecular mass of 18,800 Da and of 206 amino acid with a molecular mass of 23,659 Da, respectively. Database searching with the ORF7 and ORF8 showed no significant similarity with any other

10 proteins. Nevertheless, these genes were of similar in size and location as those observed in the sequence of other closteroviruses, BYV (P20, P21), BYSV (P18, P22), and LChV (P21, P27) (Figure 7). However, conserved regions were not observed between the ORF7 or ORF8 and its counterparts in BYV, BYSV, and LChV.

The 3' terminal untranslated region (3'-UTR) consists of 216 nucleotides.

15 Nucleotide sequence analysis revealed a long oligo(A) tract close to the end of the GLRaV-2 genome which is similar to that observed in the genome of BYV and BYSV (Agranovsky et al. "Nucleotide Sequence of the 3'-Terminal Half of Beet Yellow Closterovirus RNA Genome Unique Arrangement of Eight Virus Genes," *J. General Virology* 72:15-24 (1991); Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome

20 and Implications for the Evolution of Closteroviruses," *Virology* 221:199-207 (1996), both of which are hereby incorporated by reference). The genome of BYV ends in CCC, BYSV, and CTV ends in CC with an additional G or A in the double-stranded replicative form of BYSV (Karasev et al., "Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses," *Virology* 221:199-207 (1996), which

25 is hereby incorporated by reference) and CTV (Karasev et al., "Complete Sequence of the Citrus Tristeza Virus RNA Genome," *Virology* 208:511-20 (1995), which is hereby incorporated by reference), respectively. GLRaV-2 had CGC at the 3' terminus of the genome. Recently, a conserved 60 nt cis-element was identified in the 3'-UTR of three monopartite closteroviruses, which included a prominent conserved stem and loop structure

30 (Karasev et al., 1996). As shown in Figure 10, alignment of the 3'-UTR sequence of GLRaV-2 with the same regions of BYV, BYSV, and CTV showed the presence of the same conserved 60 nt stretch. Besides this cis-element, conserved sequences were not found in the 3' UTRs of GLRaV-2, BYV, BYSV, and CTV.

The closteroviruses studied so far (e.g., BYV, BYSV, CTV, LIYV, LChV, and GLRaV-3) have apparent similarities in genome organization, which include replication associated genes that consist of MT, HEL, and RdRP conserved domains and a five-gene array unique for closteroviruses (Dolja et al. "Molecular Biology and Evolution of Closteroviruses: Sophisticated Build-up of Large RNA Genomes," Annual Rev. Photopathology 32:261-85 (1994); Agranovsky "Principles of Molecular Organization, Expression, and Evolution of Closteroviruses: Over the Barriers," Adv. in Virus Res. 47:119-218 (1996); Jelkmann et al., "Complete Genome Structure and Phylogenetic Analysis of Little Cherry Virus, a Mealybug-Transmissible Closterovirus," J. General Virology 78:2067-71 (1997); Ling et al., "Nucleotide Sequence of the 3' Terminal Two-Thirds of the Grapevine Leafroll Associated Virus-3 Genome Reveals a Typical Monopartite Closterovirus," J. General Virology 79(5):1289-1301 (1998), all of which are hereby incorporated by reference).

The above data clearly shows that GLRaV-2 is a closterovirus. In the genome of GLRaV-2, two putative papain-like proteases were identified and an autoproteolytic cleavage process was predicted. The replication associated proteins consisting of MT, HEL, and RdRP conserved motifs were also identified, which were phylogenetically closely related to the replication associated proteins of other closteroviruses. A unique gene array including a small hydrophobic transmembrane protein, HSP70 homolog, HSP90 homolog, diverged CP and CP was also preserved in GLRaV-2. In addition, the calculated molecular mass (21,661 Da) of the coat protein (ORF6) of GLRaV-2 is in good agreement with that of the other closteroviruses (22 to 28 kDa) (Martelli and Bar-Joseph, "Closteroviruses: Classification and Nomenclature of Viruses," Fifth Report of the International Committee on Taxonomy of Viruses, Francki et al., eds., Springer-Verlag Wein, New York, p. 345-47 (1991); Candresse and Martelli, "Genus *Closterovirus*," in Virus Taxonomy. Report of the International Committee on Taxonomy of Viruses, Murphy et al., eds., Springer-Verlag., NY, p. 461-63 (1995), both of which are hereby incorporated by reference). Two ORFs downstream of the CP are of similar, in size and location, to those observed in the genome of BYV. Furthermore, lack of a poly(A) tail at the 3' end of GLRaV-2 is also in good agreement with other closteroviruses. Like all other closteroviruses, the expression of ORF1b is suspected to occur via a +1 ribosomal frameshift and the 3'proximal ORFs are probably expressed via formation of a nested set of subgenomic RNAs. Since the slippery sequence, stem-loop and pseudoknot structure involved in the frameshift of BYV were absent in GLRaV-2, the +1 frameshift of GLRaV-2 might be the same as proposed for CTV (Karasev et al., "Complete

Sequence of the Citrus Tristeza Virus RNA Genome,” Virology 208:511-20 (1995), which is hereby incorporated by reference) and BYSV (Karasev et al., “Organization of the 3'-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses,” Virology 221:199-207 (1996), which is hereby incorporated by reference).

5 Overall, GLRaV-2 is more closely related to monopartite closteroviruses BYV, BYSV, and CTV than to GLRaV-3 (Figure 7) (Ling et al., “Nucleotide Sequence of the 3' Terminal Two-Thirds of the Grapevine Leafroll Associated Virus-3 Genome Reveals a Typical Monopartite Closterovirus,” J. General Virology 79(5):1289-1301 (1998), which is hereby incorporated by reference), even though the latter causes similar leafroll symptoms in
10 grapevine (Rosciglione and Gugerli, “Maladies de l'Enroulement et du Bois Strie de la Vigne: Analyse Microscopique et Serologique (Leafroll and Stem Pitting of Grapevine: Microscopical and Serological Analysis),” Rev Suisse Viticult Arboricult Horticulture 18:207-11 (1986); Hu et al., “Characterization of Closterovirus-Like Particles Associated with Grapevine Leafroll Disease,” J. Phytopathology 128:1-14 (1990), both of which are
15 hereby incorporated by reference).

Closteroviruses are a diverse group with complex and heterogeneous genome organizations. So far, GLRaV-2 is the only closterovirus that matches with the genome organization of BYV, the type member of the genus *Closterovirus*. In addition, the genomic RNA of GLRaV-2 is about the same size as that of BYV; however, the transmission vector of
20 GLRaV-2 is unknown. The genome organization of GLRaV-2 is more closely related to the aphid transmissible closteroviruses (BYV and CTV) than to whitefly (LIYV) or mealybug transmissible closteroviruses (LChV and GLRaV-3). Thus, it is possible that GLRaV-2 is transmitted by aphids. Aphid transmission experiments with GLRaV-2 should provide information that might help develop methods for further control of GLRaV-2.

25 A total of 15,500 nucleotides or over 95% of the estimated GLRaV-2 genome has been cloned and sequenced. GLRaV-2 and GLRaV-3 (Ling et al., “Nucleotide Sequence of the 3' Terminal Two-Thirds of the Grapevine Leafroll Associated Virus-3 Genome Reveals a Typical Monopartite Closterovirus,” J. General Virology 79(5):1289-1301 (1998), which is hereby incorporated by reference) are the first grapevine leafroll associated
30 closteroviruses that have been almost completely sequenced. The above data clearly justify the inclusion of GLRaV-2 into the genus *Closterovirus*. In addition, the information regarding the genome of GLRaV-2 would provide a better understanding of this and related GLRaVs, and add fundamental knowledge to the group of closteroviruses.

Example 7 - Construction of the CP Gene of GLRaV-2 in Plant Expression Vector

GLRaV-2 infected *Vitis vinifera*, cv Pinot Noir grapevines originated from a vineyard in central New York was used as the virus isolate, from which the cp gene of GLRaV-2 was identified. Based on the sequence information, two oligonucleotide primers have been designed. The sense primer CP-96F (SEQ. ID. No. 21) starts from the ATG initiation codon of the coat protein gene and the complementary primer CP-96R (SEQ. ID. No. 22) starts from 56 nucleotides downstream of the stop codon of the CP gene. A Nco I restriction site (11 bp in SEQ. ID. No. 21 and 13 bp in SEQ. ID. No. 22) is introduced in the beginning of both primers to facilitate the cloning. The coat protein gene of GLRaV-2 was amplified from dsRNA extracted from GLRaV-2 infected grapevine using reverse transcriptase polymerase chain reaction (RT-PCR). The PCR-amplified CP product was purified from low melting temperature agarose gel, digested with Nco I and cloned into the same enzyme digested plant expression vector pEPT8 (shown at Figure 11). After screening, the orientation of recombinant construct was checked by using the internal restriction site of the CP gene and directly sequencing the CP gene. The recombinant construct with translatable (sense) full length coat protein gene, pEPT8CP-GLRaV2, was going through for the further cloning. The plant expression cassette, which consisted of a double cauliflower mosaic virus (CaMV) 35S-enhancer, a CaMV 35S-promoter, an alfalfa mosaic virus (ALMV) RNA4 5' leader sequence, a coat protein gene of GLRaV-2 (CP-GLRaV-2), and a CaMV 35S 3' untranslated region as a terminator, was cut using the EcoR I restriction enzyme, isolated from low melting point temperature agarose gel, and cloned into the same restriction enzyme treated binary vector pGA482GG or pGA482G (a derivative of pGA482 (An et al., "Binary Vectors," in *Plant Molecular Biology Manual*, pp. A3:1-19, Gelvin and Schilperoot, eds., Kluwer Academic Publishers, Dordrecht, Netherlands (1988), which is hereby incorporated by reference). The resulting recombinants constructs are pGA482GG/EPT8CP-GLRaV2 (shown at Figure 11A), which contain both neomycin phosphotransferase (npt II) and β -glucuronidase (GUS) at the internal region of the T-DNA, and pGA482G/EPT8CP-GLRaV2 (shown at Figure 11B) without GUS. These recombinants constructs were separately introduced by electroporation into disarmed avirulent *Agrobacterium tumefaciens* strain C58Z707. The *Agrobacterium tumefaciens* containing the vector was used to infect *Nicotiana benthamiana* wounded leaf disks according to the procedure essentially described by Horsch et al., "A Simple and General Method for

Transferring Genes into Plants,” Science 277:1229-1231 (1985), which is incorporated herein by reference.

Example 8 - Analysis of Transgenic *Nicotiana benthamiana* Plants with the CP Gene of GLRaV-2

NPT II-ELISA: Double-antibody sandwich enzyme linked immnuosorbent assay (DAS-ELISA) was used to detect the npt II enzyme with an NPT II-ELISA kit (5' prime to 3' prime, Inc., Boulder, Co.).

Indirect ELISA: Polyclonal antibodies to GLRaV-2, which were prepared from the coat protein expressed in *E. coli*, were used. Plates were coated with homogenized samples in extraction buffer (1:10, w/v) (phosphate buffered saline containing 0.05% Tween 20 and 2% polyvinyl pyrrolidone) and incubated overnight at 4°C. After washing with phosphate buffered saline containing 0.05% Tween 20 (PBST), the plates were blocked with blocking buffer (phosphate buffered saline containing 2% BSA) and incubated at room temperature for 1 hr. The anti-GLRaV-2 IgG was added at 2 µg/ml after washing with PBST. After incubation at 30 C for 4 hr, the plates were washed with PBST, and the goat anti-rabbit IgG conjugate of alkaline phosphatase (Sigma) was added at 1:10,000 dilution. The absorbance was measured at 405 nm with a MicroELISA AutoReader. In addition, Western blot was also performed according to the method described by Hu et al., “Characterization of Closterovirus-like Particle Associated Grapevine Leafroll Disease,” J. Phytopathology 128:1-14, (1990), which is incorporated herein by reference.

PCR analysis: Genomic DNA was extracted from leaves of putative transgenic and non-transgenic plants according to the method described by Cheung et al., “A Simple and Rapid DNA Microextraction Method for Plants, Animal, and Insect Suitable for RAPD and other PCR analysis,” PCR Methods and Applications 3:69 (1996), which is incorporated herein by reference. The extracted total DNA served as the template for PCR reaction. The primers CP-96F and CP-96R (SEQ. ID. Nos. 21 and 22, respectively) for the CP gene of GLRaV-2, as well as npt II 5'- and 3'- primers were used for PCR analysis. PCR reaction was performed at the 94°C x 3 min for one cycle, followed by 30 cycles of 94° C x 1 min, 50° C x 1 min, and 72° C x 2:30 min with an additional extension at 72° C for 10 min. The PCR product was analyzed on agarose gel.

After transformation, a total of 42 kanamycin resistant *Nicotiana benthamiana* lines (R₀) were obtained, of which the leaf samples were tested by NPT II enzyme activity.

Among them, 37 lines were NPT II positive by ELISA, which took about 88.0% of total transformants. However, some of NPT II negative plants were obtained among these selected kanamycin resistant plants. All of the transgenic plants were self-pollinated in a greenhouse, and the seeds from these transgenic lines were germinated for further analysis.

5 The production of GLRaV-2 CP in transgenic plants was detected by indirect ELISA prior to inoculation, and the results showed that GLRaV-2 CP gene expression was not detectable in all transgenic plants tested. This result was further confirmed with Western blot. Using the antibody to GLRaV-2, the production of the CP was not detected in the transgenic and nontransgenic control plants. However, a protein of expected size (~22 kDa)
10 was detected in GLRaV-2 infected positive control plants. This result was consistent with the ELISA result. The presence of the CP gene of GLRaV-2 in transgenic plants was detected from total genomic DNA extracted from plants tissue by PCR analysis (Figure 12). The DNA product of expected size (653 bp) was amplified from twenty tested transgenic lines, but not in non-transgenic plants. The result indicated that the CP gene of GLRaV-2 was present at
15 these transgenic lines, which was also confirmed by Northern blot analysis.

Example 9 - R₁ and R₂ transgenic *Nicotiana benthamiana* Plants Are Resistant to GLRaV-2

20 Inoculation of transgenic plants: GLRaV-2 isolate 94/970, which was originally identified and transmitted from grapevine to *Nicotiana benthamiana* in South Africa (Goszczynski et al., "Detection of Two Strains of Grapevine Leafroll-Associated Virus 2," *Vitis* 35:133-35 (1996), which is incorporated herein by reference), was used as inoculum. The CP gene of isolate 94/970 was sequenced; and it is identical to the CP gene
25 used in construction. *Nicotiana benthamiana* is an experimental host of GLRaV-2. The infection on it produces chlorotic and occasional necrotic lesions followed by systemic vein clearing. The vein clearing results in vein necrosis. Eventually the infected plants died, starting from the top to the bottom.

 At five to seven leaf stage, two youngest apical leaves were challenged with
30 GLRaV-2 isolate 94/970. Inoculum was prepared by grinding 1.0 g GLRaV-2 infected *Nicotiana benthamiana* leaf tissue in 5 ml of phosphate buffer (0.01M K₂HPO₄, PH7.0). The tested plants were dusted with carborundum and rubbed with the prepared inoculum. Non-transformed plants were simultaneously inoculated as above. The plants were observed for symptom development every other day for 60 days after inoculation. Resistant R₁ transgenic

plants were carried on to R2 generation for further evaluation.

Transgenic progenies from 20 R₀ lines were initially screened for the resistance to GLRaV-2 followed by inoculation with GLRaV-2 isolate 94/970. The seedlings of the transgenic plants (NPT II positive), and nontransformed control plants were inoculated with GLRaV-2. After inoculation, the reaction of tested plants were divided into three types: highly susceptible (i.e. typical symptoms were observed two to four weeks postinoculation); tolerant (i.e. no symptom was developed in the early stage and typical symptoms was shown four to eight weeks postinoculation); and resistant (i.e. the plants remained asymptomatic eight weeks postinoculation). Based on the plant reaction, the resistant plants were obtained from fourteen different lines (listed in Table 1 below). In each of these fourteen lines, there was no virus detected within these plants by ELISA at 6 weeks postinoculation. In contrast, GLRaV-2 was detected in symptomatic plants by indirect ELISA. In the other six lines, although there were a few plants with some kind of delay in symptom development, all the inoculated transgenic plants died at three to eight weeks postinoculation. Based on the initial screening results, five representative lines consisting of three resistant lines (1, 4, and 19) and two susceptible lines (12 and 13) were selected for the further analysis.

Table 1

No. Line	No.	Reaction of Tested Plants		
		HS	T	HR
line 1	39	14	3	22
line 2	36	7	6	23
line 3	38	11	4	23
line 4	31	4	5	22
line 5	33	6	13	14
line 6	36	4	16	16
line 7	32	5	9	18
line 8	37	22	9	6
line 9	36	9	12	15
line 10	14	13	1	0
line 11	13	11	2	0
line 12	17	16	1	0
line 13	16	14	0	0
line 14	17	17	0	0
line 15	32	30	2	0
line 16	33	6	13	14
line 17	12	0	1	11
line 19	15	0	0	15
line 20	19	3	0	16
line 21	14	1	3	10
control	15	15	0	0

Table 1

		Reaction of Tested Plants		
No. Line	No.	HS	T	HR
No Line: include transgenic lines and nontransformed control;				
No: the number of transgenic and nontransformed plants;				
HS: highly susceptible, typical symptoms were observed two to four weeks after inoculation;				
T: tolerant, the symptoms were observed five to eight weeks after inoculation; and				
HR: plants remain without asymptomatic after eight weeks inoculation.				

Table 2 below shows the symptom development in transgenic plants relative to non-transgenic control plants in the five selected lines in separate experiments. Non-transgenic control plants were all infected two to four weeks after inoculation, which showed typical GLRaV-2 symptoms on *Nicotiana benthamiana*, including chlorotic and local lesions followed by systemic vein clearing and vein necrosis on the leaves. Three of the tested lines (1, 4, and 19) showed some resistance that was manifested by either an absence or a delay in symptom development. Two other lines, 12 and 13, developed symptoms at nearly the same time as the non-transformed control plants. From top to bottom, the leaves of infected plants gradually became yellow, wilted, and dried, and, eventually, the whole plants died. No matter when infection occurred, the eventual result was the same. Six weeks after inoculation, all non-transgenic plants and the susceptible plants were dead. Some tolerant plants started to die. In contrast, the asymptomatic plants were flowering normally and pollinating as the non-inoculated healthy control plants (Figure 13).

Table 2

No. Line	No.	Reaction of Tested Plants		
		HS	T	HR
line 1	19	5	6	8
line 4	15	9	1	5
line 12	16	14	2	0
line 13	18	13	5	0
line 19	13	10	0	3
non-transgenic	24	23	1	0
No. Line: include transgenic lines and nontransformed control;				
No.: Number of transgenic and nontransformed plants tested;				
HS: highly susceptible; typical symptoms were observed two to four weeks after inoculation;				
T: tolerant, the symptoms were observed five to eight weeks postinoculation; and				
HR: plants remain without asymptomatic after eight weeks inoculation.				

ELISA was performed at 6 weeks postinoculation to test the GLRaV-2 replication in the plants. Presumably, the increased level of CP reflected virus replication. The result showed that the absorbance value in symptomatic plants reached (OD) 0.7 to 3.2,

compared to (OD) 0.10-0.13 prior to inoculation. In contrast, GLRaV-2 was not detected in asymptomatic plants, of which the absorbance value was the same or nearly the same as that of healthy nontransformed control plants. The data confirmed that virus replicated in symptomatic plants, but not in asymptomatic plants. The replication of GLRaV-2 was suppressed in asymptomatic plants. This result implicated that another mechanism other than the CP-mediated resistance was probably involved.

Three R2 progenies derived from transgenic resistant plants of lines 1, 4, and 19 were generated and utilized to examine the stable transmission and whether resistance was maintained in R2 generation. These results are shown in Table 3 below. NPT II analysis revealed that R2 progeny were still segregating. The CP expression in R2 progeny was still undetectable. After inoculation, all the nontransgenic plants were infected and showed GLRaV-2 symptoms on the leaves after 24 days postinoculation. In contrast, the inoculated transgenic R₂ progeny showed different levels of resistance from those highly susceptible to highly resistant. The tolerant and resistant plants were manifested by a delay in symptom development and absence of symptoms, respectively. At 6 weeks postinoculation, GLRaV-2 was detected in the tolerant symptomatic infected plants by indirect ELISA; but not in asymptomatic plants. This result indicated that virus replication was suppressed in these resistant plants, which was confirmed by Western blot. These resistant plants remained asymptomatic eight weeks postinoculation, and they were flowering normally and pollinating.

Table 3

No. Line	No. Plants	NPT II positive/negative	HS	Reaction of Tested Plants	
				T	HR
line 1/22	12	12/20	3	3	6
line 1/30	11	8/3	7	2	2
line 1/31	11	10/1	6	3	2
line 1/35	10	10/0	4	6	0
line 1/41	8	7/1	2	2	4
line 4/139	12	11/1	4	4	3
line 4/149	10	7/3	4	5	1
line 4/152	10	8/2	9	0	1
line 4/174	9	8/1	4	0	4
line 19/650	11	10/1	7	0	2
line 19/657	12	12/0	6	2	4
line 19/659	12	8/4	5	2	5
line 19/660	10	8/2	3	6	1
non-transformed CK	12	0/12	12	0	0

HS: highly susceptible, typical symptoms were observed two to four weeks after inoculation;

T: tolerant, the symptoms were observed five to eight weeks postinoculation; and

HR: plants remain asymptomatic at eight weeks postinoculation.

Example 10 - Evidence for RNA-Mediated Protection in Transgenic Plants

Northern blot analysis: Total RNA was extracted from leaves prior to inoculation following the method described by Napoli et al., Plant Cell 2:279-89 (1990), which is hereby incorporated by reference. The concentration of the extracted RNA was measured by spectrophotometer at OD 260. About 10 µg of total RNA was used for each sample. The probe used was the 3' one third of GLRaV-2 CP gene, which was randomly labeled with ³²P (α-dATP) using Klenow fragment of DNA polymerase I.

Using a DNA corresponding to the 3' one third CP gene sequence as probe, a single band was detected in the RNA extracted from susceptible plants from R1 progeny of lines 5, 12, and 13 by Northern hybridization. There was little or no signal detected in the transgenic plants from R1 progeny of line 1, 4, and 19. This RNA is not present in nontransformed control plants. The size of the hybridization signal was estimated to an approximately 0.9 kb nucleic acid, which was about the same as estimated (Figure 14). In lines of 1, 4, and 19, the steady state level of RNA expression was also low in R2 progeny. This data showed that susceptible plants from lines 12 and 13 had high mRNA level and all transgenic plants from lines 1, 4, and 19 had low mRNA level.

Example 11 - Transformation and Analysis of Transgenic Grapevines with the CP Gene of GLRaV-2

Plant materials: The rootstock cultivars Couderc 3309 (3309C) (*V. riparia* x *V. rupestris*), *Vitis riparia* 'Gloire de Montpellier' (Gloire), Teleki 5C (5C) (*V. berlandieri* x *V. riparia*), Millardet et De Grasset 101-14 (101-14 MGT) (*V. riparia* x *V. rupestris*), and Richter 110 (110R) (*V. rupestris* x *V. berlandieri*) were utilized. Initial embryogenic calli of Gloire were provided by Mozsar and Süle (Plant Protection Institute, Hungarian Academy of Science, Budapest). All other plant materials came from a vineyard at the New York State Agricultural Experiment Station, Geneva, NY. Buds were removed from the clusters and surface sterilized in 70% ethanol for 1-2 min. The buds (from the greenhouse and the field) were transferred to 1% sodium hypochlorite for 15 min, then rinsed three times in sterile, double-distilled water. Anthers were excised aseptically from flower buds with the aid of a stereo microscope. The pollen was crushed on a microscope slide under a coverslip with a drop of acetocarmine to observe the cytological stage. This was done to determine which stage was most favorable for callus induction.

Somatic embryogenesis and regeneration: Anthers were plated under aseptic conditions at a density of 40 to 50 per 9 cm diameter Petri dish containing MSE. Plates were cultured at 28°C in the dark. Callus was initiated, and, after 60 days, embryos were induced and were transferred to hormone-free HMG medium for differentiation. Torpedo stage embryos were then transferred from HMG to MGC medium to promote embryo germination. Cultures were maintained in the dark at 26-28°C and transferred to fresh medium at 3-4 week intervals. Elongated embryos were transferred to rooting medium in baby food jars (5-8 embryos per jar). The embryos were grown in a tissue culture room at 25°C with a daily 16 h photoperiod (76 :mol. s) to induce shoot and root formation. After plants developed roots, they were transplanted to soil in the greenhouse.

Transformation: The protocols used for transformation were modified from those described by Scorza et.al., "Transformation of Grape (*Vitis vinifera* L.) Zygotic-derived Somatic Embryos and Regeneration of Transgenic Plants," Plant Cell Rpt. 14:589-92 (1995), which is hereby incorporated by reference. Overnight cultures of *Agrobacterium* strain C58Z707 or LBA4404 were grown in LB medium at 28°C in a shaking incubator. Bacteria were centrifuged for 5 min at 3000-5000 rpm and resuspended in MS liquid medium (OD 1.0 at A600 nm). Calli with embryos were immersed in the bacterial suspension for 15-30 min, blotted dry, and transferred to HMG medium with or without acetosyringone (100 µM). Embryogenic calli were co-cultivated with the bacteria for 48 h in the dark at 28°C. Then, the plant material was washed in MS liquid plus cefotaxime (300 mg/ml) and carbenicillin (200 mg/ml) 2-3 times. To select transgenic embryos, the material was transferred to HMG medium containing either 20 or 40 mg/L kanamycin, 300 mg/L cefotaxime, and 200 mg/L carbenicillin. Alternatively, after co-cultivation, embryogenic calli were transferred to initiation MSE medium containing 25 mg/l kanamycin plus the same antibiotics listed above. All plant materials were incubated in continuous dark at 28°C. After growth on selection medium for 3 months, embryos were transferred to HMG or MGC without kanamycin to promote elongation of embryos. They were then transferred to rooting medium without antibiotics. Nontransformed calli were grown on the same media with and without kanamycin to verify the efficiency of the kanamycin selection process.

Although the invention has been described in detail for the purpose of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cornell Research Foundation, Inc.
- (ii) TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS TYPE 2 PROTEINS
AND THEIR USES
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 - (B) STREET: Clinton Square, P.O. Box 1051
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 14603
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/047,194
 - (B) FILING DATE: 20-MAY-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Goldman, Michael L.
 - (B) REGISTRATION NUMBER: 30,727
 - (C) REFERENCE/DOCKET NUMBER: 19603/1632
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (716) 263-1304
 - (B) TELEFAX: (716) 263-1600

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAACATTGC GAGAGAACCC CATTAGCGTC TCCGGGGTGA ACTTGGAAG GTCTGCCGCC	60
GCTCAGGTTA TTTATTTCGG CAGTTTCACG CAGCCCTTCG CGTTGTATCC GCGCCAAGAG	120
AGCGCGATCG TAAAAACGCA ACTTCCACCG GTCAGTGTAG TGAAGGTGGA GTGCGTAGCT	180
GCGGAGGTAG CTCCCACAG GGGCGTGGTC GACAAGAAAC CTACGTCTGT TGGCGTTCCC	240
CCGCAGCGCG GTGTGCTTTC TTTTCCGACG GTGGTTCGGA ACCGCGGCGA CGTGATAATC	300
ACAGGGGTGG TGCATGAAGC CCTGAAGAAA ATTAAAGACG GGCTCTTACG CTTCCGCGTA	360
GGCGGTGACA TGCCTTTTTT GAGATTTTTT TCATCGAACT ACGGCTGCAG ATTCGTGCGG	420
AGCGTGCCTA CGAACACTAC AGTTTGGCTA AATTGCACGA AAGCGAGTGG TGAGAAATTC	480
TCACTCGCCG CCGCGTGCAC GCGGATTAC GTGGCGATGC TGCCTTATGT GTGTGGCGGG	540
AAATTTCCAC TCGTCCCTCAT GAGTAGAGTT ATTTACCCGG ATGGGCGCTG TTAATTGGCC	600
CATATGAGGT ATTTGTGCGC CTTTTACTGT CGCCCGTTTA GAGAGTCGGA TTATGCCCTC	660
GGAATGTGGC CTACGGTGGC GCGTCTCAGG GCATGCGTTG AGAAGAACTT CGGTGTCGAA	720
GCTTGTGGCA TAGCTCTTCG TGGCTATTAC ACCTCTCGCA ATGTTTATCA CTGTGATTAT	780
GAATCTGCTT ATGTAAAATA TTTTAGAAAC CTTTCCGGCC GCATTGGCGG TGGTTCGTTC	840
GATCCGACAT CTTTAACCTC CGTAATAACG GTGAAGATTA GCGGTCTTCC AGGTGGTCTT	900
CCTAAAATA TAGCGTTTGG TGCCTTCCTG TCGGATATAC GTTACGTCGA ACCGGTAGAC	960
TCGGGCGGCA TTCAATCGAG CGTTAAGACG AAACGTGAAG ATGCGCACCG AACCGTAGAG	1020
GAACGGGCGG CCGGCGGATC CGTCGAGCAA CCGCGACAAA AGAGGATAGA TGAGAAAGGT	1080
TGCGGCAGAG TTCCTAGTGG AGGTTTTTCG CATCTCCTGG TCGGCAACCT TAACGAAGTT	1140
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ATGACTAGAA TTAGATACCC GAACGGGTTT TGTTACTTGG CTCACTGCCG GTACGCGTGC	1440
GCGTTTCTCT TAAGGGGTTT TGATCCGAAG CGTTTCGACA TCGGTGCTTT CCCCACCGCG	1500
GCCAAGCTCA GAAACCGTAT GGTTCGGAG CTTGGTGAAA GAAGTTTAGG TTTGAACTTG	1560
TACGGCGCAT ATACGTCAG CGGCGTCTTT CACTGCGATT ATGACGCTAA GTTTATAAAG	1620

GATTTGCGTC TTATGTCAGC AGTTATAGCT GGAAAGGACG GGGTGAAGA GGTGGTACCT	1680
TCTGACATAA CTCCTGCCAT GAAGCAGAAA ACGATCGAAG CCGTGTATGA TAGATTATAT	1740
GGCGGCACTG ACTCGTTGCT GAAACTGAGC ATCGAGAAAG ACTTAATCGA TTTCAAAAAT	1800
GACGTGCAGA GTTTGAAGAA AGATCGGCCG ATTGTCAAAG TGCCCTTTTA CATGTCGGAA	1860
GCAACACAGA ATTCGCTGAC GCGTTTCTAC CCTCAGTTTCG AACTTAAGTT TTCGCACTCC	1920
TCGCATTAGC ATCATCCCGC CGCCGCCGCT TCTAGACTGC TGGAAAATGA AACGTTAGTG	1980
CGCTTATGTG GTAATAGCGT TTCAGATATT GGAGGTTGTC CTCTTTTCCA TTTGCATTCC	2040
AAGACGCAAA GACGGGTTCA CGTATGTAGG CCTGTGTTGG ATGGCAAGGA TGCAGCGCT	2100
CGCGTGGTGC GTGATTTGCA GTATTCCAAC GTGCGTTTGG GAGACGATGA TAAAATTTTG	2160
GAAGGGCCAC GCAATATCGA CATTGTCAC TATCCTCTGG GCGCGTGTGA CCACGAAAGT	2220
AGTGCTATGA TGATGGTGCA GGTGTATGAC GCGTCCCTTT ATGAGATATG TGGCGCCATG	2280
ATCAAGAAGA AAAGCCGCAT AACGTACTTA ACCATGGTCA CGCCCGGCGA GTTCTTTGAC	2340
GGACGCGAAT GCGTCTACAT GGAGTCGTTA GACTGTGAGA TTGAAGTTGA TGTGCACGCG	2400
GACGTCGTAA TGTACAAATT CGGTAGTTCT TGCTATTCGC ACAAGCTTTC AATCATCAAG	2460
GACATCATGA CCACTCCGTA CTTGACACTA GGTGGTTTTTC TATTCAGCGT GGAGATGTAT	2520
GAGGTGCGTA TGGGCGTGAA TTAATTCAAG ATTACGAAGT CCGAAGTATC GCCTAGCATT	2580
AGCTGCACCA AGCTCCTGAG ATACCGAAGA GCTAATAGTG ACGTGGTTAA AGTTAAACTT	2640
CCACGTTTTCG ATAAGAAACG TCGCATGTGT CTGCCTGGGT ATGACACCAT ATACCTAGAT	2700
TCGAAGTTTG TGAGTCGCGT TTTCGATTAT GTCGTGTGTA ATTGCTCTGC CGTGAAGTCA	2760
AAAACTTTCG AGTGGGTGTG GAGTTTCATT AAGTCTAGTA AGTCGAGGGT GATTATTAGC	2820
GGTAAAATAA TTCACAAGGA TGTGAATTTG GACCTCAAGT ACGTCGAGAG TTTCGCCGCG	2880
GTTATGTTGG CCTCTGGCGT GCGCAGTAGA CTAGCGTCCG AGTACCTTGC TAAGAACCTT	2940
AGTCATTTTT CGGGAGATTG CTCCTTTATT GAAGCCACGT CTTTCGTGTT GCGTGAGAAA	3000
ATCAGAAACA TGAATCTGAA TTTTAACGAA AGACTTTTAC AGTTAGTGAA GCGCGTTGCC	3060
TTTGCGACCT TGGACGTGAG TTTTCTAGAT TTAGATTCAA CTCTTGAATC AATAACTGAT	3120
TTTGCCGAGT GTAAGGTAGC GATTGAACTC GACGAGTTGG GTTGCTTGAG AGCGGAGGCC	3180
GAGAATGAAA AAATCAGGAA TCTGGCGGGA GATTGATTG CGGCTAAACT CGCGAGCGAG	3240
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AACGCCGATA	AGCGGGAAGT	TCAGAGGCC	GGTTTGCGTG	GTGGTTCTAG	AAACGGGGTT	3360
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GATCAACAAC	GGATCAAGTC	TTACGTGCGT	TTCTTGGA	CGGCGGTCTC	ATTCTTGGAT	3480
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TTCGCGTTTT	TGGCGAATCG	CGGCGACTTA	TCTAGTCGTG	TCCGTAGCGC	GGTGTGTGCT	3600
GTGAAAGAAG	TTGCTACCTC	ATGCGCGAAC	GCGAGCGTTT	CTAAAGCCAA	GGTTATGATT	3660
ACCTTCGCAG	CGGCCGTGTG	TGCTATGATG	TTTAATAGCT	GCGGTTTTTC	AGGCGACGGT	3720
CGGGAGTATA	AATCGTATAT	ACATCGTTAC	ACGCAAGTAT	TGTTTGACAC	TATCTTTTTT	3780
GAGGACAGCA	GTTACCTACC	CATAGAAGTT	CTGAGTTCGG	CGATATGCGG	TGCTATCGTC	3840
ACACTTTTCT	CCTCGGGCTC	GTCCATAAGT	TTAAACGCCT	TCTTACTTCA	AATTACCAAA	3900
GGATTCTCCC	TAGAGGTTGT	CGTCCGGAAT	GTTGTGCGAG	TCACGCATGG	TTTGAGCACC	3960
ACAGCGACCG	ACGGCGTCAT	ACGTGGGGTT	TTCTCCCAAA	TTGTGTCTCA	CTTACTTGTT	4020
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GTAAAAAGT	GTGTGAGCTT	AATCTTCATC	TTGCGTGAAG	ATACTTATTC	CGGTTTTATT	4140
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AAAGAAGCTA	CTCAGGAAGC	GATTCGTACG	ACGGTCATGC	AAGTGCCTGT	CGCTGTAGTG	4320
GATGCCCTTA	AGAGCGCCGC	GGGAAAAATT	TATAACAATT	TTAGTAGTCG	ACGTACCTTT	4380
GGTAAGGATG	AAGGCTCCTC	TAGCGACGGC	GCATGTGAAG	AGTATTTCTC	ATGCGACGAA	4440
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GACTTTTACC	TCCTTTAAAG	ACTTAACCTC	CGATTTTAAC	GACGAGCGCT	TAATTCAAAA	9060
GCTCGCTGAA	CTTGTGGCTT	TAAAATATGA	GGTTCAAACC	GGCAACACCA	CCTTGGCGTT	9120
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CAGGTTATTT ATTTCCGCGAG TTTCACGCAG CCCTTCGCGT TGTATCCGCG CCAAGAGAGC	120
GCGATCGTAA AAACGCAACT TCCACCGGTC AGTGTAAGTG AGGTGGAGTG CGTAGCTGCG	180
GAGGTAGCTC CCGACAGGGG CGTGGTCGAC AAGAAACCTA CGTCTGTTGG CGTTCCCCCG	240
CAGCGCGGTG TGCTTTCTTT TCCGACGGTG GTTCGGAACC GCGGCGACGT GATAATCACA	300
GGGGTGGTGC ATGAAGCCCT GAAGAAAATT AAAGACGGGC TCTTACGCTT CCGCGTAGGC	360
GGTGACATGC GTTTTTCGAG ATTTTTCTCA TCGAACTACG GCTGCAGATT CGTCGCGAGC	420
GTGCGTACGA AACTACAGT TTGGCTAAAT TGCACGAAAG CGAGTGGTGA GAAATTCTCA	480
CTCGCCGCCG CGTGACCGGC GGATTACGTG GCGATGCTGC GTTATGTGTG TGGCGGGAAA	540
TTTCCACTCG TCCTCATGAG TAGAGTTATT TACCCGATG GCGCTGTTA CTTGGCCCAT	600
ATGAGGTATT TGTGCGCCTT TACTGTCTGC CCGTTTAGAG AGTCGGATTA TGCCCTCGGA	660
ATGTGGCCTA CCGTGGCGCG TCTCAGGGCA TCGGTTGAGA AGAACTTCGG TGTCGAAGCT	720
TGTGGCATAG CTCTTCGTGG CTATTACACC TCTCGCAATG TTTATCACTG TGATTATGAC	780
TCTGCTTATG TAAATATTT TAGAAACCTT TCCGGCCGCA TTGGCGGTGG TTCGTTCGAT	840
CCGACATCTT TAACCTCCGT AATAACGGTG AAGATTAGCG GTCTTCCAGG TGGTCTTCCT	900
AAAAATATAG CGTTTGGTGC CTTCTGTGC GATATACGTT ACGTCGAACC GGTAGACTCG	960
GGCGGCATTC AATCGAGCGT TAAGACGAAA CGTGAAGATG CGCACCGAAC CGTAGAGGAA	1020
CGGGCGGCCG GCGGATCCGT CGAGCAACCG CGACAAAAGA GGATAGATGA GAAAGGTTGC	1080

GGCAGAGTTC	CTAGTGGAGG	TTTTTCGCAT	CTCCTGGTCG	GCAACCTTAA	CGAAGTTAGG	1140
AGGAAGGTAG	CTGCCGGACT	TCTACGCTTT	CGCGTTGGCG	GTGATATGGA	TTTTCATCGC	1200
TCGTTCTCCA	CCCAAGCGGG	CCACCGCTTG	CTGGTGTGGC	GCCGCTCGAG	CCGGAGCGTG	1260
TGCCTTGAAC	TTTACTCACC	ATCTAAAAAC	TTTTTGCGTT	ACGATGTCTT	GCCCTGTTCT	1320
GGAGACTATG	CAGCGATGTT	TTCTTTCGCG	GCGGGCGGCC	GTTTCCCTTT	AGTTTTGATG	1380
ACTAGAATTA	GATACCCGAA	CGGGTTTTGT	TACTTGGCTC	ACTGCCGGTA	CGCGTGC GCG	1440
TTTCTCTTAA	GGGGTTTTGA	TCCGAAGCGT	TTCGACATCG	GTGCTTTCCC	CACCGCGGCC	1500
AAGCTCAGAA	ACCGTATGGT	TTCGGAGCTT	GGTGAAAGAA	GTTTAGGTTT	GAAGTTGTAC	1560
GGCGCATATA	CGTCACGCGG	CGTCTTTCAC	TGCGATTATG	ACGCTAAGTT	TATAAAGGAT	1620
TTGCGTCTTA	TGTCAGCAGT	TATAGCTGGA	AAGGACGGGG	TGGAAGAGGT	GGTACCTTCT	1680
GACATAACTC	CTGCCATGAA	GCAGAAAACG	ATCGAAGCCG	TGTATGATAG	ATTATATGGC	1740
GGCACTGACT	CGTTGCTGAA	ACTGAGCATC	GAGAAAGACT	TAATCGATTT	CAAAAATGAC	1800
GTGCAGAGTT	TGAAGAAAGA	TCGGCCGATT	GTCAAAGTGC	CCTTTTACAT	GTCGGAAGCA	1860
ACACAGAATT	CGCTGACGCG	TTTCTACCCT	CAGTTCGAAC	TTAAGTTTTT	GCACTCCTCG	1920
CATTGAGATC	ATCCCGCCGC	CGCCGCTTCT	AGACTGCTGG	AAAATGAAAC	GTTAGTGCGC	1980
TTATGTGGTA	ATAGCGTTTC	AGATATTGGA	GGTTGTCCTC	TTTTCCATTT	GCATTCCAAG	2040
ACGCAAAGAC	GGGTTACAGT	ATGTAGGCCT	GTGTTGGATG	GCAAGGATGC	GCAGCGTCGC	2100
GTGGTGCGTG	ATTTGCAGTA	TTCCAACGTG	CGTTTGGGAG	ACGATGATAA	AATTTTGGAA	2160
GGGCCACGCA	ATATCGACAT	TTGCCACTAT	CCTCTGGGCG	CGTGTGACCA	CGAAAGTAGT	2220
GCTATGATGA	TGGTGCAGGT	GTATGACGCG	TCCCTTTATG	AGATATGTGG	CGCCATGATC	2280
AAGAAGAAAA	GCCGCATAAC	GTACTTAACC	ATGGTCACGC	CCGGCGAGTT	TCTTGACGGA	2340
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GTCGTAATGT	ACAAATTCGG	TAGTTCTTGC	TATTCGCACA	AGCTTTCAAT	CATCAAGGAC	2460
ATCATGACCA	CTCCGTACTT	GACACTAGGT	GGTTTTCTAT	TCAGCGTGGA	GATGTATGAG	2520
GTGCGTATGG	GCGTGAATTA	CTTCAAGATT	ACGAAGTCCG	AAGTATCGCC	TAGCATTAGC	2580
TGCACCAAGC	TCCTGAGATA	CCGAAGAGCT	AATAGTGACG	TGGTTAAAGT	TAAACTTCCA	2640
CGTTTCGATA	AGAAACGTCG	CATGTGTCTG	CCTGGGTATG	ACACCATATA	CCTAGATTCG	2700
AAGTTTGTGA	GTCGCGTTTT	CGATTATGTC	GTGTGTAATT	GCTCTGCCGT	GAAGTCAAAA	2760

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CATTTTTTCGG	GAGATTGCTC	CTTTATTGAA	GCCACGTCTT	TCGTGTTGCG	TGAGAAAATC	3000
AGAAACATGA	CTCTGAATTT	TAACGAAAGA	CTTTTACAGT	TAGTGAAGCG	CGTTGCCTTT	3060
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GCCGAGTGTA	AGGTAGCGAT	TGAACTCGAC	GAGTTGGGTT	GCTTGAGAGC	GGAGGCCGAG	3180
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GCCGATAAGC	GGGAAGTTCA	GAGGCCCGGT	TTGCGTGGTG	GTTCTAGAAA	CGGGGTTGTT	3360
GGGGAGTTCC	TTCACTTCGT	CGTGGATTCT	GCCTTGCGTC	TTTTCAAATA	CGCGACGGAT	3420
CAACAACGGA	TCAAGTCTTA	CGTGCGTTTC	TTGGA CT CGG	CGGTCTCATT	CTTGGATTAC	3480
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GCGTTTTTTGG	CGAATCGCGG	CGACTTATCT	AGTCGTGTCC	GTAGCGCGGT	GTGTGCTGTG	3600
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GAGTATAAAT	CGTATATACA	TCGTTACACG	CAAGTATTGT	TTGACACTAT	CTTTTTTGAG	3780
GACAGCAGTT	ACCTACCCAT	AGAAGTTCTG	AGTTCGGCGA	TATGCGGTGC	TATCGTCACA	3840
CTTTTCTCCT	CGGGCTCGTC	CATAAGTTTA	AACGCCTTCT	TACTTCAAAT	TACCAAAGGA	3900
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GCGACCGACG	GCGTCATACG	TGGGGTTTTT	TCCCAAATTG	TGTCTCACTT	ACTTGTTGGA	4020
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AAAAAGTGTG	TGAGCTTAAT	CTTCATCTTG	CGTGAAGATA	CTTATTCCGG	TTTTATTAAG	4140
CACGGAATCA	GTGAATTCTC	TTTCCTTAGT	AGTATTCTGA	AGTTCTTGAA	GGGTAAGCTT	4200
GTGGACGAGT	TGAAATCGAT	TATTCAAGGG	GTTTTTGATT	CCAACAAGCA	CGTGTTTAAA	4260
GAAGCTACTC	AGGAAGCGAT	TCGTACGACG	GTCATGCAAG	TGCCTGTCGC	TGTAGTGGAT	4320
GCCCTTAAGA	GCGCCGCGGG	AAAAATTTAT	AACAATTTTA	CTAGTCGACG	TACCTTTGGT	4380
AAGGATGAAG	GCTCCTCTAG	CGACGGCGCA	TGTGAAGAGT	ATTTCTCATG	CGACGAAGGT	4440
GAAGGTCCGG	GTCTGAAAGG	GGGTTCCAGC	TATGGCTTCT	CAATTTTAGC	GTTCTTTTCA	4500

CGCATTATGT	GGGGAGCTCG	TCGGCTTATT	GTTAAGGTGA	AGCATGAGTG	TTTTGGGAAA	4560
CTTTTTGAAT	TTCTATCGCT	CAAGCTTCAC	GAATTCAGGA	CTCGCGTTTT	TGGAAGAAT	4620
AGAACGGACG	TGGGAGTTTA	CGATTTTTTG	CCCACGGGCA	TCGTGGAAAC	GCTCTCATCG	4680
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GCTTCGTTGA	CCGATATGAA	TTACTTTGAG	TTCTCAGAAG	ACTTCTTAGC	CTCTATCGAG	4800
GAGCCGCCTT	TCGCTGGATT	GCGAGGAGGT	AGCAAGAACA	TCGCGATTTT	GGCGATTTTG	4860
GAATACGCGC	ATAATTTGTT	TCGCATTGTC	GCAAGCAAGT	GTTCGAAACG	ACCTTTATTT	4920
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AAGAGCCAGC	TCGTCGCTAT	CGTGCGCGAG	TATACTCAGA	GATTCCTCCG	AAGTCGCATG	5040
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TTAATGAAGC	GGAAGGTTTC	AGGTTTCGTT	TTAGCTAGTG	TTTATCGCCC	ACTTAGAGGT	5160
TTCTCATATA	TGTGTGTTTC	AGCGGAGCGA	CGTGAAAAGT	TTTTTGCTCT	CGTGTGTTTA	5220
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GTGTCCTCAG	CGCGTCGCTT	TTATGAGCGT	ATTAAAATTT	TTCTAAGGCA	GAAGTATGTC	5340
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GCAGGGTTGA	AAGGTGGTGC	GTCGCGAATG	ACGCTCTTCC	ACCTTCTGGT	TCGCCTTGCT	5460
AGTGCCCTCC	TATCGTTAGG	GTGGGAAGGG	TTAAAGCTAC	TCTTATCGCA	CCACAAGTTG	5520
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CCTCGCGCGC	CTGCACTACT	CAAAGGGTTT	TTTGAGTGCG	TGGCGAACAG	CACTGTGTCA	5760
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GGGTTGCGTG	CGGATGGTAG	GGGTCTCCAT	CGGCAGAAAG	CCGTACCCGT	CATACCTTCT	5880
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AGACGCAGAA	ATCGTGACAC	TAATGACGAC	GAATTTACGC	GCCCTGCTCA	TGAGCAGATG	6060
CAAGAAGTCA	CCACTTTCTG	TTCGAAAGCC	AACTCTGCTG	GTTTGGCCCT	GGAAAGGGCA	6120
GTGCTTGTGG	AAGACGCTAT	AAAGTCGGAG	AACTTTTCTA	AGACGGTTAA	TGAGATGGTG	6180

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GAAGAAATCT	CTGTTGCTGA	CGAGCGAGAC	GATTCGCCTA	AGACAGTCAG	GATAAGCGAA	6300
TACCTAAATA	GGTTAAACTC	AAGCTTCGAA	TTCCCGAAGC	CTATTGTTGT	GGACGACAAC	6360
AAGGATACCG	GGGGTCTAAC	GAACGCCGTG	AGGGAGTTTT	ATTATATGCA	AGAACTTGCT	6420
CTTTTCGAAA	TCCACAGCAA	ACTGTGCACC	TACTACGATC	AACTGCGCAT	AGTCAACTTC	6480
GATCGTTCCG	TAGCACCATG	CAGCGAAGAT	GCTCAGCTGT	ACGTACGGAA	GAACGGCTCA	6540
ACGATAGTGC	AGGGTAAAGA	GGTACGTTTG	CACATTAAGG	ATTTCCACGA	TCACGATTTC	6600
CTGTTTGACG	GAAAAATTTT	TATTAACAAG	CGGCGGCGAG	GCGGAAATGT	TTTATATCAC	6660
GACAACCTCG	CGTTCTTGGC	GAGTAATTTG	TTCTTAGCCG	GCTACCCCTT	TTCAAGGAGC	6720
TTCGTCTTCA	CGAATTCGTC	GGTCGATATT	CTCCTCTACG	AAGCTCCACC	CGGAGGTGGT	6780
AAGACGACGA	CGCTGATTGA	CTCGTTCTTG	AAGGTCTTCA	AGAAAGGTGA	GGTTTCCACC	6840
ATGATCTTAA	CCGCCAACAA	AAGTTCGCAG	GTTGAGATCC	TAAAGAAAGT	GGAGAAGGAA	6900
GTGTCTAACA	TTGAATGCCA	GAAACGTAAA	GACAAAAGAT	CTCCGAAAAA	GAGCATTTAC	6960
ACCATCGACG	CTTATTTAAT	GCATCACCGT	GGTTGTGATG	CAGACGTTCT	TTTCATCGAT	7020
GAGTGTTCAT	TGGTTCATGC	GGGTAGCGTA	CTAGCTTGCA	TTGAGTTCAC	GAGGTGTCAT	7080
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TCAGTCGACG	ATTTAGTCCC	CGACGTGGGT	TCCACGTTTC	TGTGTATGCT	TCAGTCGGAG	7380
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AGCTTAACTT	ATAACGTCTT	AGCTGCTCGT	CGAGGTGACG	CCACTTGCGA	TGCCATCCAG	7620
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TTTGGTGATT	TGTCCGCGGA	CTTCAGTACT	GGGCCTTTTG	AGTGCGGTGC	CAGCGGTATT	7860
GTGGTGCGGG	ACAACATCTC	CTCCAGCAAC	ATCACTGATC	ACGATAAGCA	GCGTGTTTAG	7920

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2639 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Thr Leu Arg Glu Asn Pro Ile Ser Val Ser Gly Val Asn Leu Gly Arg
1           5           10           15

Ser Ala Ala Ala Gln Val Ile Tyr Phe Gly Ser Phe Thr Gln Pro Phe
          20           25           30

Ala Leu Tyr Pro Arg Gln Glu Ser Ala Ile Val Lys Thr Gln Leu Pro
          35           40           45

Pro Val Ser Val Val Lys Val Glu Cys Val Ala Ala Glu Val Ala Pro
          50           55           60

Asp Arg Gly Val Val Asp Lys Lys Pro Thr Ser Val Gly Val Pro Pro
65           70           75           80

Gln Arg Gly Val Leu Ser Phe Pro Thr Val Val Arg Asn Arg Gly Asp
          85           90           95

Val Ile Ile Thr Gly Val Val His Glu Ala Leu Lys Lys Ile Lys Asp
          100          105          110

Gly Leu Leu Arg Phe Arg Val Gly Gly Asp Met Arg Phe Ser Arg Phe
          115          120          125

Phe Ser Ser Asn Tyr Gly Cys Arg Phe Val Ala Ser Val Arg Thr Asn
          130          135          140

Thr Thr Val Trp Leu Asn Cys Thr Lys Ala Ser Gly Glu Lys Phe Ser
145          150          155          160

Leu Ala Ala Ala Cys Thr Ala Asp Tyr Val Ala Met Leu Arg Tyr Val
          165          170          175

Cys Gly Gly Lys Phe Pro Leu Val Leu Met Ser Arg Val Ile Tyr Pro
          180          185          190

Asp Gly Arg Cys Tyr Leu Ala His Met Arg Tyr Leu Cys Ala Phe Tyr
          195          200          205

Cys Arg Pro Phe Arg Glu Ser Asp Tyr Ala Leu Gly Met Trp Pro Thr
          210          215          220

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Val	Ala	Arg	Leu	Arg	Ala	Cys	Val	Glu	Lys	Asn	Phe	Gly	Val	Glu	Ala	225	230	235	240
Cys	Gly	Ile	Ala	Leu	Arg	Gly	Tyr	Tyr	Thr	Ser	Arg	Asn	Val	Tyr	His	245	250	255	
Cys	Asp	Tyr	Asp	Ser	Ala	Tyr	Val	Lys	Tyr	Phe	Arg	Asn	Leu	Ser	Gly	260	265	270	
Arg	Ile	Gly	Gly	Gly	Ser	Phe	Asp	Pro	Thr	Ser	Leu	Thr	Ser	Val	Ile	275	280	285	
Thr	Val	Lys	Ile	Ser	Gly	Leu	Pro	Gly	Gly	Leu	Pro	Lys	Asn	Ile	Ala	290	295	300	
Phe	Gly	Ala	Phe	Leu	Cys	Asp	Ile	Arg	Tyr	Val	Glu	Pro	Val	Asp	Ser	305	310	315	320
Gly	Gly	Ile	Gln	Ser	Ser	Val	Lys	Thr	Lys	Arg	Glu	Asp	Ala	His	Arg	325	330	335	
Thr	Val	Glu	Glu	Arg	Ala	Ala	Gly	Gly	Ser	Val	Glu	Gln	Pro	Arg	Gln	340	345	350	
Lys	Arg	Ile	Asp	Glu	Lys	Gly	Cys	Gly	Arg	Val	Pro	Ser	Gly	Gly	Phe	355	360	365	
Ser	His	Leu	Leu	Val	Gly	Asn	Leu	Asn	Glu	Val	Arg	Arg	Lys	Val	Ala	370	375	380	
Ala	Gly	Leu	Leu	Arg	Phe	Arg	Val	Gly	Gly	Asp	Met	Asp	Phe	His	Arg	385	390	395	400
Ser	Phe	Ser	Thr	Gln	Ala	Gly	His	Arg	Leu	Leu	Val	Trp	Arg	Arg	Ser	405	410	415	
Ser	Arg	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Ser	Pro	Ser	Lys	Asn	Phe	Leu	420	425	430	
Arg	Tyr	Asp	Val	Leu	Pro	Cys	Ser	Gly	Asp	Tyr	Ala	Ala	Met	Phe	Ser	435	440	445	
Phe	Ala	Ala	Gly	Gly	Arg	Phe	Pro	Leu	Val	Leu	Met	Thr	Arg	Ile	Arg	450	455	460	
Tyr	Pro	Asn	Gly	Phe	Cys	Tyr	Leu	Ala	His	Cys	Arg	Tyr	Ala	Cys	Ala	465	470	475	480
Phe	Leu	Leu	Arg	Gly	Phe	Asp	Pro	Lys	Arg	Phe	Asp	Ile	Gly	Ala	Phe	485	490	495	
Pro	Thr	Ala	Ala	Lys	Leu	Arg	Asn	Arg	Met	Val	Ser	Glu	Leu	Gly	Glu	500	505	510	
Arg	Ser	Leu	Gly	Leu	Asn	Leu	Tyr	Gly	Ala	Tyr	Thr	Ser	Arg	Gly	Val	515	520	525	

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Phe His Cys Asp Tyr Asp Ala Lys Phe Ile Lys Asp Leu Arg Leu Met
 530 535 540

Ser Ala Val Ile Ala Gly Lys Asp Gly Val Glu Glu Val Val Pro Ser
 545 550 555 560

Asp Ile Thr Pro Ala Met Lys Gln Lys Thr Ile Glu Ala Val Tyr Asp
 565 570 575

Arg Leu Tyr Gly Gly Thr Asp Ser Leu Leu Lys Leu Ser Ile Glu Lys
 580 585 590

Asp Leu Ile Asp Phe Lys Asn Asp Val Gln Ser Leu Lys Lys Asp Arg
 595 600 605

Pro Ile Val Lys Val Pro Phe Tyr Met Ser Glu Ala Thr Gln Asn Ser
 610 615 620

Leu Thr Arg Phe Tyr Pro Gln Phe Glu Leu Lys Phe Ser His Ser Ser
 625 630 635 640

His Ser Asp His Pro Ala Ala Ala Ala Ser Arg Leu Leu Glu Asn Glu
 645 650 655

Thr Leu Val Arg Leu Cys Gly Asn Ser Val Ser Asp Ile Gly Gly Cys
 660 665 670

Pro Leu Phe His Leu His Ser Lys Thr Gln Arg Arg Val His Val Cys
 675 680 685

Arg Pro Val Leu Asp Gly Lys Asp Ala Gln Arg Arg Val Val Arg Asp
 690 695 700

Leu Gln Tyr Ser Asn Val Arg Leu Gly Asp Asp Asp Lys Ile Leu Glu
 705 710 715 720

Gly Pro Arg Asn Ile Asp Ile Cys His Tyr Pro Leu Gly Ala Cys Asp
 725 730 735

His Glu Ser Ser Ala Met Met Met Val Gln Val Tyr Asp Ala Ser Leu
 740 745 750

Tyr Glu Ile Cys Gly Ala Met Ile Lys Lys Lys Ser Arg Ile Thr Tyr
 755 760 765

Leu Thr Met Val Thr Pro Gly Glu Phe Leu Asp Gly Arg Glu Cys Val
 770 775 780

Tyr Met Glu Ser Leu Asp Cys Glu Ile Glu Val Asp Val His Ala Asp
 785 790 795 800

Val Val Met Tyr Lys Phe Gly Ser Ser Cys Tyr Ser His Lys Leu Ser
 805 810 815

Ile Ile Lys Asp Ile Met Thr Thr Pro Tyr Leu Thr Leu Gly Gly Phe
 820 825 830

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Leu Phe Ser Val Glu Met Tyr Glu Val Arg Met Gly Val Asn Tyr Phe
 835 840 845
 Lys Ile Thr Lys Ser Glu Val Ser Pro Ser Ile Ser Cys Thr Lys Leu
 850 855 860
 Leu Arg Tyr Arg Arg Ala Asn Ser Asp Val Val Lys Val Lys Leu Pro
 865 870 875 880
 Arg Phe Asp Lys Lys Arg Arg Met Cys Leu Pro Gly Tyr Asp Thr Ile
 885 890 895
 Tyr Leu Asp Ser Lys Phe Val Ser Arg Val Phe Asp Tyr Val Val Cys
 900 905 910
 Asn Cys Ser Ala Val Asn Ser Lys Thr Phe Glu Trp Val Trp Ser Phe
 915 920 925
 Ile Lys Ser Ser Lys Ser Arg Val Ile Ile Ser Gly Lys Ile Ile His
 930 935 940
 Lys Asp Val Asn Leu Asp Leu Lys Tyr Val Glu Ser Phe Ala Ala Val
 945 950 955 960
 Met Leu Ala Ser Gly Val Arg Ser Arg Leu Ala Ser Glu Tyr Leu Ala
 965 970 975
 Lys Asn Leu Ser His Phe Ser Gly Asp Cys Ser Phe Ile Glu Ala Thr
 980 985 990
 Ser Phe Val Leu Arg Glu Lys Ile Arg Asn Met Thr Leu Asn Phe Asn
 995 1000 1005
 Glu Arg Leu Leu Gln Leu Val Lys Arg Val Ala Phe Ala Thr Leu Asp
 1010 1015 1020
 Val Ser Phe Leu Asp Leu Asp Ser Thr Leu Glu Ser Ile Thr Asp Phe
 1025 1030 1035 1040
 Ala Glu Cys Lys Val Ala Ile Glu Leu Asp Glu Leu Gly Cys Leu Arg
 1045 1050 1055
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 1060 1065 1070
 Ala Ala Lys Leu Ala Ser Glu Ile Val Val Asp Ile Asp Ser Lys Pro
 1075 1080 1085
 Ser Pro Lys Gln Val Gly Asn Ser Ser Ser Glu Asn Ala Asp Lys Arg
 1090 1095 1100
 Glu Val Gln Arg Pro Gly Leu Arg Gly Gly Ser Arg Asn Gly Val Val
 1105 1110 1115 1120
 Gly Glu Phe Leu His Phe Val Val Asp Ser Ala Leu Arg Leu Phe Lys
 1125 1130 1135

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Tyr Ala Thr Asp Gln Gln Arg Ile Lys Ser Tyr Val Arg Phe Leu Asp
 1140 1145 1150
 Ser Ala Val Ser Phe Leu Asp Tyr Asn Tyr Asp Asn Leu Ser Phe Ile
 1155 1160 1165
 Leu Arg Val Leu Ser Glu Gly Tyr Ser Cys Met Phe Ala Phe Leu Ala
 1170 1175 1180
 Asn Arg Gly Asp Leu Ser Ser Arg Val Arg Ser Ala Val Cys Ala Val
 1185 1190 1195 1200
 Lys Glu Val Ala Thr Ser Cys Ala Asn Ala Ser Val Ser Lys Ala Lys
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 Val Met Ile Thr Phe Ala Ala Ala Val Cys Ala Met Met Phe Asn Ser
 1220 1225 1230
 Cys Gly Phe Ser Gly Asp Gly Arg Glu Tyr Lys Ser Tyr Ile His Arg
 1235 1240 1245
 Tyr Thr Gln Val Leu Phe Asp Thr Ile Phe Phe Glu Asp Ser Ser Tyr
 1250 1255 1260
 Leu Pro Ile Glu Val Leu Ser Ser Ala Ile Cys Gly Ala Ile Val Thr
 1265 1270 1275 1280
 Leu Phe Ser Ser Gly Ser Ser Ile Ser Leu Asn Ala Phe Leu Leu Gln
 1285 1290 1295
 Ile Thr Lys Gly Phe Ser Leu Glu Val Val Val Arg Asn Val Val Arg
 1300 1305 1310
 Val Thr His Gly Leu Ser Thr Thr Ala Thr Asp Gly Val Ile Arg Gly
 1315 1320 1325
 Val Phe Ser Gln Ile Val Ser His Leu Leu Val Gly Asn Thr Gly Asn
 1330 1335 1340
 Val Ala Tyr Gln Ser Ala Phe Ile Ala Gly Val Val Pro Leu Leu Val
 1345 1350 1355 1360
 Lys Lys Cys Val Ser Leu Ile Phe Ile Leu Arg Glu Asp Thr Tyr Ser
 1365 1370 1375
 Gly Phe Ile Lys His Gly Ile Ser Glu Phe Ser Phe Leu Ser Ser Ile
 1380 1385 1390
 Leu Lys Phe Leu Lys Gly Lys Leu Val Asp Glu Leu Lys Ser Ile Ile
 1395 1400 1405
 Gln Gly Val Phe Asp Ser Asn Lys His Val Phe Lys Glu Ala Thr Gln
 1410 1415 1420
 Glu Ala Ile Arg Thr Thr Val Met Gln Val Pro Val Ala Val Val Asp
 1425 1430 1435 1440

- 100 -

Ala Leu Lys Ser	Ala Ala Gly Lys Ile Tyr Asn Asn Phe Thr Ser Arg	
1445	1450	1455
Arg Thr Phe Gly Lys Asp Glu Gly Ser Ser Ser Asp Gly Ala Cys Glu		
1460	1465	1470
Glu Tyr Phe Ser Cys Asp Glu Gly Glu Gly Pro Gly Leu Lys Gly Gly		
1475	1480	1485
Ser Ser Tyr Gly Phe Ser Ile Leu Ala Phe Phe Ser Arg Ile Met Trp		
1490	1495	1500
Gly Ala Arg Arg Leu Ile Val Lys Val Lys His Glu Cys Phe Gly Lys		
1505	1510	1515 1520
Leu Phe Glu Phe Leu Ser Leu Lys Leu His Glu Phe Arg Thr Arg Val		
1525	1530	1535
Phe Gly Lys Asn Arg Thr Asp Val Gly Val Tyr Asp Phe Leu Pro Thr		
1540	1545	1550
Gly Ile Val Glu Thr Leu Ser Ser Ile Glu Glu Cys Asp Gln Ile Glu		
1555	1560	1565
Glu Leu Leu Gly Asp Asp Leu Lys Gly Asp Lys Asp Ala Ser Leu Thr		
1570	1575	1580
Asp Met Asn Tyr Phe Glu Phe Ser Glu Asp Phe Leu Ala Ser Ile Glu		
1585	1590	1595 1600
Glu Pro Pro Phe Ala Gly Leu Arg Gly Gly Ser Lys Asn Ile Ala Ile		
1605	1610	1615
Leu Ala Ile Leu Glu Tyr Ala His Asn Leu Phe Arg Ile Val Ala Ser		
1620	1625	1630
Lys Cys Ser Lys Arg Pro Leu Phe Leu Ala Phe Ala Glu Leu Ser Ser		
1635	1640	1645
Ala Leu Ile Glu Lys Phe Lys Glu Val Phe Pro Arg Lys Ser Gln Leu		
1650	1655	1660
Val Ala Ile Val Arg Glu Tyr Thr Gln Arg Phe Leu Arg Ser Arg Met		
1665	1670	1675 1680
Arg Ala Leu Gly Leu Asn Asn Glu Phe Val Val Lys Ser Phe Ala Asp		
1685	1690	1695
Leu Leu Pro Ala Leu Met Lys Arg Lys Val Ser Gly Ser Phe Leu Ala		
1700	1705	1710
Ser Val Tyr Arg Pro Leu Arg Gly Phe Ser Tyr Met Cys Val Ser Ala		
1715	1720	1725
Glu Arg Arg Glu Lys Phe Phe Ala Leu Val Cys Leu Ile Gly Leu Ser		
1730	1735	1740

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Leu Pro Phe Phe Val Arg Ile Val Gly Ala Lys Ala Cys Glu Glu Leu
 1745 1750 1755 1760

Val Ser Ser Ala Arg Arg Phe Tyr Glu Arg Ile Lys Ile Phe Leu Arg
 1765 1770 1775

Gln Lys Tyr Val Ser Leu Ser Asn Phe Phe Cys His Leu Phe Ser Ser
 1780 1785 1790

Asp Val Asp Asp Ser Ser Ala Ser Ala Gly Leu Lys Gly Gly Ala Ser
 1795 1800 1805

Arg Met Thr Leu Phe His Leu Leu Val Arg Leu Ala Ser Ala Leu Leu
 1810 1815 1820

Ser Leu Gly Trp Glu Gly Leu Lys Leu Leu Leu Ser His His Asn Leu
 1825 1830 1835 1840

Leu Phe Leu Cys Phe Ala Leu Val Asp Asp Val Asn Val Leu Ile Lys
 1845 1850 1855

Val Leu Gly Gly Leu Ser Phe Phe Val Gln Pro Ile Phe Ser Leu Phe
 1860 1865 1870

Ala Ala Met Leu Leu Gln Pro Asp Arg Phe Val Glu Tyr Ser Glu Lys
 1875 1880 1885

Leu Val Thr Ala Phe Glu Phe Phe Leu Lys Cys Ser Pro Arg Ala Pro
 1890 1895 1900

Ala Leu Leu Lys Gly Phe Phe Glu Cys Val Ala Asn Ser Thr Val Ser
 1905 1910 1915 1920

Lys Thr Val Arg Arg Leu Leu Arg Cys Phe Val Lys Met Leu Lys Leu
 1925 1930 1935

Arg Lys Gly Arg Gly Leu Arg Ala Asp Gly Arg Gly Leu His Arg Gln
 1940 1945 1950

Lys Ala Val Pro Val Ile Pro Ser Asn Arg Val Val Thr Asp Gly Val
 1955 1960 1965

Glu Arg Leu Ser Val Lys Met Gln Gly Val Glu Ala Leu Arg Thr Glu
 1970 1975 1980

Leu Arg Ile Leu Glu Asp Leu Asp Ser Ala Val Ile Glu Lys Leu Asn
 1985 1990 1995 2000

Arg Arg Arg Asn Arg Asp Thr Asn Asp Asp Glu Phe Thr Arg Pro Ala
 2005 2010 2015

His Glu Gln Met Gln Glu Val Thr Thr Phe Cys Ser Lys Ala Asn Ser
 2020 2025 2030

Ala Gly Leu Ala Leu Glu Arg Ala Val Leu Val Glu Asp Ala Ile Lys
 2035 2040 2045

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Ser Glu Lys Leu Ser Lys Thr Val Asn Glu Met Val Arg Lys Gly Ser
 2050 2055 2060
 Thr Thr Ser Glu Glu Val Ala Val Ala Leu Ser Asp Asp Glu Ala Val
 2065 2070 2075 2080
 Glu Glu Ile Ser Val Ala Asp Glu Arg Asp Asp Ser Pro Lys Thr Val
 2085 2090 2095
 Arg Ile Ser Glu Tyr Leu Asn Arg Leu Asn Ser Ser Phe Glu Phe Pro
 2100 2105 2110
 Lys Pro Ile Val Val Asp Asp Asn Lys Asp Thr Gly Gly Leu Thr Asn
 2115 2120 2125
 Ala Val Arg Glu Phe Tyr Tyr Met Gln Glu Leu Ala Leu Phe Glu Ile
 2130 2135 2140
 His Ser Lys Leu Cys Thr Tyr Tyr Asp Gln Leu Arg Ile Val Asn Phe
 2145 2150 2155 2160
 Asp Arg Ser Val Ala Pro Cys Ser Glu Asp Ala Gln Leu Tyr Val Arg
 2165 2170 2175
 Lys Asn Gly Ser Thr Ile Val Gln Gly Lys Glu Val Arg Leu His Ile
 2180 2185 2190
 Lys Asp Phe His Asp His Asp Phe Leu Phe Asp Gly Lys Ile Ser Ile
 2195 2200 2205
 Asn Lys Arg Arg Arg Gly Gly Asn Val Leu Tyr His Asp Asn Leu Ala
 2210 2215 2220
 Phe Leu Ala Ser Asn Leu Phe Leu Ala Gly Tyr Pro Phe Ser Arg Ser
 2225 2230 2235 2240
 Phe Val Phe Thr Asn Ser Ser Val Asp Ile Leu Leu Tyr Glu Ala Pro
 2245 2250 2255
 Pro Gly Gly Gly Lys Thr Thr Thr Leu Ile Asp Ser Phe Leu Lys Val
 2260 2265 2270
 Phe Lys Lys Gly Glu Val Ser Thr Met Ile Leu Thr Ala Asn Lys Ser
 2275 2280 2285
 Ser Gln Val Glu Ile Leu Lys Lys Val Glu Lys Glu Val Ser Asn Ile
 2290 2295 2300
 Glu Cys Gln Lys Arg Lys Asp Lys Arg Ser Pro Lys Lys Ser Ile Tyr
 2305 2310 2315 2320
 Thr Ile Asp Ala Tyr Leu Met His His Arg Gly Cys Asp Ala Asp Val
 2325 2330 2335
 Leu Phe Ile Asp Glu Cys Phe Met Val His Ala Gly Ser Val Leu Ala
 2340 2345 2350

Cys	Ile	Glu	Phe	Thr	Arg	Cys	His	Lys	Val	Met	Ile	Phe	Gly	Asp	Ser	
2355					2360					2365						
Arg	Gln	Ile	His	Tyr	Ile	Glu	Arg	Asn	Glu	Leu	Asp	Lys	Cys	Leu	Tyr	
2370					2375					2380						
Gly	Asp	Leu	Asp	Arg	Phe	Val	Asp	Leu	Gln	Cys	Arg	Val	Tyr	Gly	Asn	
2385					2390					2395					2400	
Ile	Ser	Tyr	Arg	Cys	Pro	Trp	Asp	Val	Cys	Ala	Trp	Leu	Ser	Thr	Val	
2405					2410					2415						
Tyr	Gly	Asn	Leu	Ile	Ala	Thr	Val	Lys	Gly	Glu	Ser	Glu	Gly	Lys	Ser	
2420					2425					2430						
Ser	Met	Arg	Ile	Asn	Glu	Ile	Asn	Ser	Val	Asp	Asp	Leu	Val	Pro	Asp	
2435					2440					2445						
Val	Gly	Ser	Thr	Phe	Leu	Cys	Met	Leu	Gln	Ser	Glu	Lys	Leu	Glu	Ile	
2450					2455					2460						
Ser	Lys	His	Phe	Ile	Arg	Lys	Gly	Leu	Thr	Lys	Leu	Asn	Val	Leu	Thr	
2465					2470					2475					2480	
Val	His	Glu	Ala	Gln	Gly	Glu	Thr	Tyr	Ala	Arg	Val	Asn	Leu	Val	Arg	
2485					2490					2495						
Leu	Lys	Phe	Gln	Glu	Asp	Glu	Pro	Phe	Lys	Ser	Ile	Arg	His	Ile	Thr	
2500					2505					2510						
Val	Ala	Leu	Ser	Arg	His	Thr	Asp	Ser	Leu	Thr	Tyr	Asn	Val	Leu	Ala	
2515					2520					2525						
Ala	Arg	Arg	Gly	Asp	Ala	Thr	Cys	Asp	Ala	Ile	Gln	Lys	Ala	Ala	Glu	
2530					2535					2540						
Leu	Val	Asn	Lys	Phe	Arg	Val	Phe	Pro	Thr	Ser	Phe	Gly	Gly	Ser	Val	
2545					2550					2555					2560	
Ile	Asn	Leu	Asn	Val	Lys	Lys	Asp	Val	Glu	Asp	Asn	Ser	Arg	Cys	Lys	
2565					2570					2575						
Ala	Ser	Ser	Ala	Pro	Leu	Ser	Val	Ile	Asn	Asp	Phe	Leu	Asn	Glu	Val	
2580					2585					2590						
Asn	Pro	Gly	Thr	Ala	Val	Ile	Asp	Phe	Gly	Asp	Leu	Ser	Ala	Asp	Phe	
2595					2600					2605						
Ser	Thr	Gly	Pro	Phe	Glu	Cys	Gly	Ala	Ser	Gly	Ile	Val	Val	Arg	Asp	
2610					2615					2620						
Asn	Ile	Ser	Ser	Ser	Asn	Ile	Thr	Asp	His	Asp	Lys	Gln	Arg	Val		
2625					2630					2635						

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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AGCGTAGTTC GGTGCGAGGC GATTCCGCGT AGAAAACCTT CTCTACAAGA AAATTTGTAT      60
TCGTTTGAAG CGCGGAATTA TAACTTCTCG ACTTGCGACC GTAACACATC TGCTTCAATG      120
TTCGGAGAGG CTATGGCGAT GAACTGTCTT CGTCGTTGCT TCGACCTAGA TGCCTTTTCG      180
TCCCTGCGTG ATGATGTGAT TAGTATCACA CGTTCAGGCA TCGAACAATG GCTGGAGAAA      240
CGTACTCCTA GTCAGATTAA AGCATTAATG AAGGATGTTG AATCGCCTTT GGAAATTGAC      300
GATGAAATTT GTCGTTTTAA GTTGATGGTG AAGCGTGACG CTAAGGTGAA GTTAGACTCT      360
TCTTGTTTAA CTAAACACAG CGCCGCTCAA AATATCATGT TTCATCGCAA GAGCATTAAAT      420
GCTATCTTCT CTCCTATCTT TAATGAGGTG AAAAACCGAA TAATGTGCTG TCTTAAGCCT      480
AACATAAAGT TTTTACGGA GATGACTAAC AGGGATTTTG CTTCTGTTGT CAGCAACATG      540
CTTGGTGACG ACGATGTGTA CCATATAGGT GAAGTTGATT TCTCAAAGTA CGACAAGTCT      600
CAAGATGCTT TCGTGAAGGC TTTTGAAGAA GTAATGTATA AGGAACTCGG TGTTGATGAA      660
GAGTTGCTGG CTATCTGGAT GTGCGGCGAG CGGTTATCGA TAGCTAACAC TCTCGATGGT      720
CAGTTGTCCT TCACGATCGA GAATCAAAGG AAGTCGGGAG CTTCGAACAC TTGGATTGGT      780
AACTCTCTCG TCACTTTGGG TATTTTAAGT CTTTACTACG ACGTTAGAAA TTTCGAGGCG      840
TTGTACATCT CGGGCGATGA TTCTTTAATT TTTTCTCGCA GCGAGATTTC GAATTATGCC      900
GACGACATAT GCACTGACAT GGGTTTTGAG ACAAATTTA TGTCCCAAG TGTCCCGTAC      960
TTTTGTTCTA AATTTGTTGT TATGTGTGGT CATAAGACGT TTTTGTTC CGACCCGTAC     1020
AAGCTTTTTG TCAAGTTGGG AGCAGTCAAA GAGGATGTTT CAATGGATTT CCTTTTCGAG     1080
ACTTTTACCT CCTTTAAAGA CTTAACCTCC GATTTTAACG ACGAGCGCTT AATTCAAAAG     1140
CTCGCTGAAC TTGTGGCTTT AAAATATGAG GTTCAAACCG GCAACACCAC CTTGGCGTTA     1200
AGTGTGATAC ATTGTTTGCG TTCGAATTTT CTCTCGTTTA GCAAGTTATA TCCTCGCGTG     1260
AAGGGATGGC AGGTTTTTTT CACGTCGGTT AAGAAAGCGC TTCTCAAGAG TGGGTGTTCT     1320
CTCTTCGACA GTTTCATGAC CCCTTTTGGT CAGGCTGTCA TGGTTTGGGA TGATGAGTAG     1380

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Ser Val Val Arg Ser Gln Ala Ile Pro Arg Arg Lys Pro Ser Leu Gln
1           5           10           15

Glu Asn Leu Tyr Ser Phe Glu Ala Arg Asn Tyr Asn Phe Ser Thr Cys
20           25           30

Asp Arg Asn Thr Ser Ala Ser Met Phe Gly Glu Ala Met Ala Met Asn
35           40           45

Cys Leu Arg Arg Cys Phe Asp Leu Asp Ala Phe Ser Ser Leu Arg Asp
50           55           60

Asp Val Ile Ser Ile Thr Arg Ser Gly Ile Glu Gln Trp Leu Glu Lys
65           70           75           80

Arg Thr Pro Ser Gln Ile Lys Ala Leu Met Lys Asp Val Glu Ser Pro
85           90           95

Leu Glu Ile Asp Asp Glu Ile Cys Arg Phe Lys Leu Met Val Lys Arg
100          105          110

Asp Ala Lys Val Lys Leu Asp Ser Ser Cys Leu Thr Lys His Ser Ala
115          120          125

Ala Gln Asn Ile Met Phe His Arg Lys Ser Ile Asn Ala Ile Phe Ser
130          135          140

Pro Ile Phe Asn Glu Val Lys Asn Arg Ile Met Cys Cys Leu Lys Pro
145          150          155          160

Asn Ile Lys Phe Phe Thr Glu Met Thr Asn Arg Asp Phe Ala Ser Val
165          170          175

Val Ser Asn Met Leu Gly Asp Asp Asp Val Tyr His Ile Gly Glu Val
180          185          190

Asp Phe Ser Lys Tyr Asp Lys Ser Gln Asp Ala Phe Val Lys Ala Phe
195          200          205

Glu Glu Val Met Tyr Lys Glu Leu Gly Val Asp Glu Glu Leu Leu Ala
210          215          220

Ile Trp Met Cys Gly Glu Arg Leu Ser Ile Ala Asn Thr Leu Asp Gly

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225		230		235		240									
Gln	Leu	Ser	Phe	Thr	Ile	Glu	Asn	Gln	Arg	Lys	Ser	Gly	Ala	Ser	Asn
				245					250					255	
Thr	Trp	Ile	Gly	Asn	Ser	Leu	Val	Thr	Leu	Gly	Ile	Leu	Ser	Leu	Tyr
			260					265						270	
Tyr	Asp	Val	Arg	Asn	Phe	Glu	Ala	Leu	Tyr	Ile	Ser	Gly	Asp	Asp	Ser
		275					280					285			
Leu	Ile	Phe	Ser	Arg	Ser	Glu	Ile	Ser	Asn	Tyr	Ala	Asp	Asp	Ile	Cys
	290					295					300				
Thr	Asp	Met	Gly	Phe	Glu	Thr	Lys	Phe	Met	Ser	Pro	Ser	Val	Pro	Tyr
305					310					315					320
Phe	Cys	Ser	Lys	Phe	Val	Val	Met	Cys	Gly	His	Lys	Thr	Phe	Phe	Val
				325					330					335	
Pro	Asp	Pro	Tyr	Lys	Leu	Phe	Val	Lys	Leu	Gly	Ala	Val	Lys	Glu	Asp
			340					345					350		
Val	Ser	Met	Asp	Phe	Leu	Phe	Glu	Thr	Phe	Thr	Ser	Phe	Lys	Asp	Leu
		355					360					365			
Thr	Ser	Asp	Phe	Asn	Asp	Glu	Arg	Leu	Ile	Gln	Lys	Leu	Ala	Glu	Leu
		370				375					380				
Val	Ala	Leu	Lys	Tyr	Glu	Val	Gln	Thr	Gly	Asn	Thr	Thr	Leu	Ala	Leu
385					390					395					400
Ser	Val	Ile	His	Cys	Leu	Arg	Ser	Asn	Phe	Leu	Ser	Phe	Ser	Lys	Leu
				405					410					415	
Tyr	Pro	Arg	Val	Lys	Gly	Trp	Gln	Val	Phe	Tyr	Thr	Ser	Val	Lys	Lys
			420					425					430		
Ala	Leu	Leu	Lys	Ser	Gly	Cys	Ser	Leu	Phe	Asp	Ser	Phe	Met	Thr	Pro
		435					440					445			
Phe	Gly	Gln	Ala	Val	Met	Val	Trp	Asp	Asp	Glu					
	450					455									

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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ATGAATCAGG TTTTGCAGTT TGAATGTTTG TTTCTGCTGA ATCTCGCGGT TTTTGCTGTG 60
 ACTTTTCATTT TCATTCTTCT GGTCTTCCGC GTGATTAAGT CTTTTCGCCA GAAGGGTCAC 120
 GAAGCACCTG TTCCCCTTGT TCGTGGCGGG GGTTTTTCAG CCGTAGTGTA G 171

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Gln Val Leu Gln Phe Glu Cys Leu Phe Leu Leu Asn Leu Ala
 1 5 10 15
 Val Phe Ala Val Thr Phe Ile Phe Ile Leu Leu Val Phe Arg Val Ile
 20 25 30
 Lys Ser Phe Arg Gln Lys Gly His Glu Ala Pro Val Pro Val Val Arg
 35 40 45
 Gly Gly Gly Phe Ser Thr Val Val
 50 55

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1800 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGTAGTTT TCGGTTTGGA CTTTGGCACC ACATTCTCTA CGGTGTGTGT GTACAAGGAT 60
 GGACGAGTTT TTTCATTCAA GCAGAATAAT TCGGCGTACA TCCCCACTTA CCTCTATCTC 120
 TTCTCCGATT CTAACCACAT GACTTTTGGT TACGAGGCCG AATCACTGAT GAGTAATCTG 180
 AAAGTTAAAG GTTCGTTTTA TAGAGATTTA AAACGTTGGG TGGGTTGCGA TTCGAGTAAC 240
 CTCGACGCGT ACCTTGACCG TTAAAACCT CATTACTCGG TCCGCTTGGT TAAGATCGGC 300
 TCTGGCTTGA ACGAAACTGT TTCAATTGGA AACTTCGGGG GCACTGTTAA GTCTGAGGCT 360
 CATCTGCCAG GGTTGATAGC TCTCTTTATT AAGGCTGTCA TTAGTTGCGC GGAGGGCGCG 420

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TTTGC GTGCA CTTGC ACCGG GGT TATTTGT TCAGTACCTG CCAATTATGA TAGCGTTCAA	480
AGGAATTTCA CTGATCAGTG TGTTTCACTC AGCGGTTATC AGTGCGTATA TATGATCAAT	540
GAACCTTCAG CGGCTGCGCT ATCTGCGTGT AATTCGATTG GAAAGAAGTC CGCAAATTTG	600
GCTGTTTACG ATTTTCGGTGG TGGGACCTTC GACGTGTCTA TCATTTCATA CCGCAACAAT	660
ACTTTTGTTG TGCGAGCTTC TGGAGGCGAT CTAAATCTCG GTGGAAGGGA TGTTGATCGT	720
GCGTTTCTCA CGCACCTCTT CTCTTTAACA TCGCTGGAAC CTGACCTCAC TTTGGATATC	780
TCGAATCTGA AAGAATCTTT ATCAAAAACG GACGCAGAGA TAGTTTACAC TTTGAGAGGT	840
GTCGATGGAA GAAAAGAAGA CGTTAGAGTA AACAAAAACA TTCTTACGTC GGTGATGCTC	900
CCCTACGTGA ACAGAACGCT TAAGATATTA GAGTCAACCT TAAAATCGTA TGCTAAGAGT	960
ATGAATGAGA GTGCGCGAGT TAAGTGCGAT TTAGTGCTGA TAGGAGGATC TTCATATCTT	1020
CCTGGCCTGG CAGACGTACT AACGAAGCAT CAGAGCGTTG ATCGTATCTT AAGAGTTTCG	1080
GATCCTCGGG CTGCCGTGGC CGTCGGTTGC GCATTATATT CTTCATGCCT CTCAGGATCT	1140
GGGGGGTTGC TACTGATCGA CTGTGCAGCT CACACTGTCG CTATAGCGGA CAGAA GTTGT	1200
CATCAAATCA TTTGCGCTCC AGCGGGGGCA CCGATCCCCT TTTCAGGAAG CATGCCTTTG	1260
TACTTAGCCA GGGTCAACAA GAAC TCGCAG CGTGAAGTCG CCGTGTTTGA AGGGGAGTAC	1320
GTTAAGTGCC CTAAGAACAG AAAGATCTGT GGAGCAAATA TAAGATTTTT TGATATAGGA	1380
GTGACGGGTG ATTCGTACGC ACCCGTTACC TTCTATATGG ATTTCTCCAT TTCAAGCGTA	1440
GGAGCCGTTT CATTCGTGGT GAGAGGTCCT GAGGGTAAGC AAGTG TCACT CACTGGA ACT	1500
CCAGCGTATA ACTTTTCGTC TGTGGCTCTC GGATCACGCA GTGTCCGAGA ATTGCATATT	1560
AGTTTAAATA ATAAAGTTTT TCTCGGTTTG CTTCTACATA GAAAGGCGGA TCGACGAATA	1620
CTTTTCACTA AGGATGAAGC GATTCGATAC GCCGATTCAA TTGATATCGC GGATGTGCTA	1680
AAGGAATATA AAAGTTACGC GGCCAGTGCC TTACCACCAG ACGAGGATGT CGAATTACTC	1740
CTGGGAAAGT CTGTTCAAAA AGTTTTACGG GGAAGCAGAC TGGAAGAAAT ACCTCTCTAG	1800

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Val	Val	Phe	Gly	Leu	Asp	Phe	Gly	Thr	Thr	Phe	Ser	Thr	Val	Cys	1	5	10	15
Val	Tyr	Lys	Asp	Gly	Arg	Val	Phe	Ser	Phe	Lys	Gln	Asn	Asn	Ser	Ala	20	25	30	
Tyr	Ile	Pro	Thr	Tyr	Leu	Tyr	Leu	Phe	Ser	Asp	Ser	Asn	His	Met	Thr	35	40	45	
Phe	Gly	Tyr	Glu	Ala	Glu	Ser	Leu	Met	Ser	Asn	Leu	Lys	Val	Lys	Gly	50	55	60	
Ser	Phe	Tyr	Arg	Asp	Leu	Lys	Arg	Trp	Val	Gly	Cys	Asp	Ser	Ser	Asn	65	70	75	80
Leu	Asp	Ala	Tyr	Leu	Asp	Arg	Leu	Lys	Pro	His	Tyr	Ser	Val	Arg	Leu	85	90	95	
Val	Lys	Ile	Gly	Ser	Gly	Leu	Asn	Glu	Thr	Val	Ser	Ile	Gly	Asn	Phe	100	105	110	
Gly	Gly	Thr	Val	Lys	Ser	Glu	Ala	His	Leu	Pro	Gly	Leu	Ile	Ala	Leu	115	120	125	
Phe	Ile	Lys	Ala	Val	Ile	Ser	Cys	Ala	Glu	Gly	Ala	Phe	Ala	Cys	Thr	130	135	140	
Cys	Thr	Gly	Val	Ile	Cys	Ser	Val	Pro	Ala	Asn	Tyr	Asp	Ser	Val	Gln	145	150	155	160
Arg	Asn	Phe	Thr	Asp	Gln	Cys	Val	Ser	Leu	Ser	Gly	Tyr	Gln	Cys	Val	165	170	175	
Tyr	Met	Ile	Asn	Glu	Pro	Ser	Ala	Ala	Ala	Leu	Ser	Ala	Cys	Asn	Ser	180	185	190	
Ile	Gly	Lys	Lys	Ser	Ala	Asn	Leu	Ala	Val	Tyr	Asp	Phe	Gly	Gly	Gly	195	200	205	
Thr	Phe	Asp	Val	Ser	Ile	Ile	Ser	Tyr	Arg	Asn	Asn	Thr	Phe	Val	Val	210	215	220	
Arg	Ala	Ser	Gly	Gly	Asp	Leu	Asn	Leu	Gly	Gly	Arg	Asp	Val	Asp	Arg	225	230	235	240
Ala	Phe	Leu	Thr	His	Leu	Phe	Ser	Leu	Thr	Ser	Leu	Glu	Pro	Asp	Leu	245	250	255	
Thr	Leu	Asp	Ile	Ser	Asn	Leu	Lys	Glu	Ser	Leu	Ser	Lys	Thr	Asp	Ala	260	265	270	
Glu	Ile	Val	Tyr	Thr	Leu	Arg	Gly	Val	Asp	Gly	Arg	Lys	Glu	Asp	Val	275	280	285	

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Arg	Val	Asn	Lys	Asn	Ile	Leu	Thr	Ser	Val	Met	Leu	Pro	Tyr	Val	Asn	
290						295					300					
Arg	Thr	Leu	Lys	Ile	Leu	Glu	Ser	Thr	Leu	Lys	Ser	Tyr	Ala	Lys	Ser	
305					310					315					320	
Met	Asn	Glu	Ser	Ala	Arg	Val	Lys	Cys	Asp	Leu	Val	Leu	Ile	Gly	Gly	
				325					330					335		
Ser	Ser	Tyr	Leu	Pro	Gly	Leu	Ala	Asp	Val	Leu	Thr	Lys	His	Gln	Ser	
			340					345					350			
Val	Asp	Arg	Ile	Leu	Arg	Val	Ser	Asp	Pro	Arg	Ala	Ala	Val	Ala	Val	
	355						360					365				
Gly	Cys	Ala	Leu	Tyr	Ser	Ser	Cys	Leu	Ser	Gly	Ser	Gly	Gly	Leu	Leu	
	370					375					380					
Leu	Ile	Asp	Cys	Ala	Ala	His	Thr	Val	Ala	Ile	Ala	Asp	Arg	Ser	Cys	
385					390					395					400	
His	Gln	Ile	Ile	Cys	Ala	Pro	Ala	Gly	Ala	Pro	Ile	Pro	Phe	Ser	Gly	
				405					410					415		
Ser	Met	Pro	Leu	Tyr	Leu	Ala	Arg	Val	Asn	Lys	Asn	Ser	Gln	Arg	Glu	
			420					425					430			
Val	Ala	Val	Phe	Glu	Gly	Glu	Tyr	Val	Lys	Cys	Pro	Lys	Asn	Arg	Lys	
	435						440					445				
Ile	Cys	Gly	Ala	Asn	Ile	Arg	Phe	Phe	Asp	Ile	Gly	Val	Thr	Gly	Asp	
	450					455					460					
Ser	Tyr	Ala	Pro	Val	Thr	Phe	Tyr	Met	Asp	Phe	Ser	Ile	Ser	Ser	Val	
465					470					475					480	
Gly	Ala	Val	Ser	Phe	Val	Val	Arg	Gly	Pro	Glu	Gly	Lys	Gln	Val	Ser	
				485					490					495		
Leu	Thr	Gly	Thr	Pro	Ala	Tyr	Asn	Phe	Ser	Ser	Val	Ala	Leu	Gly	Ser	
			500					505					510			
Arg	Ser	Val	Arg	Glu	Leu	His	Ile	Ser	Leu	Asn	Asn	Lys	Val	Phe	Leu	
	515						520					525				
Gly	Leu	Leu	Leu	His	Arg	Lys	Ala	Asp	Arg	Arg	Ile	Leu	Phe	Thr	Lys	
	530					535					540					
Asp	Glu	Ala	Ile	Arg	Tyr	Ala	Asp	Ser	Ile	Asp	Ile	Ala	Asp	Val	Leu	
545					550					555					560	
Lys	Glu	Tyr	Lys	Ser	Tyr	Ala	Ala	Ser	Ala	Leu	Pro	Pro	Asp	Glu	Asp	
				565					570					575		
Val	Glu	Leu	Leu	Leu	Gly	Lys	Ser	Val	Gln	Lys	Val	Leu	Arg	Gly	Ser	
			580					585						590		

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Arg Leu Glu Glu Ile Pro Leu
595

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGTCGAATT ACTCCTGGGA AAGTCTGTTC AAAAAGTTTT ACGGGGAAGC AGACTGGAAG	60
AAATACCTCT CTAGGAGCAT AGCAGCACAC TCAAGTGAAA TTAAACTCTT ACCAGACATT	120
CGATTGTACG GCGGTAGGGT TGTAAAGAAG TCCGAATTCG AATCAGCACT TCCTAATTCT	180
TTTGAACAGG AATTAGGACT GTTCATACTG AGCGAACGGG AAGTGGGATG GAGCAAATTA	240
TGCGGAATAA CGGTGGAAGA AGCAGCATA C GATCTTACGA ATCCCAAGGC TTATAAATTC	300
ACTGCCGAGA CATGTAGCCC GGATGTAAAA GGTGAAGGAC AAAAATACTC TATGGAAGAC	360
GTGATGAATT TCATGCGTTT ATCAAATCTG GATGTTAACG ACAAGATGCT GACGGAACAG	420
TGTTGGTCGC TGTCCAATTC ATGCGGTGAA TTGATCAACC CAGACGACAA AGGGCGATTC	480
GTGGCTCTCA CCTTTAAGGA CAGAGACACA GCTGATGACA CGGGTGCCGC CAACGTGGAA	540
TGTCGCGTGG GCGACTATCT AGTTTACGCT ATGTCCCTGT TTGAGCAGAG GACCCAAAAA	600
TCGCAGTCTG GCAACATCTC TCTGTACGAA AAGTACTGTG AATACATCAG GACCTACTTA	660
GGGAGTACAG ACCTGTTCTT CACAGCGCCG GACAGGATTC CGTTACTTAC GGGCATCCTA	720
TACGATTTTT GTAAGGAATA CAACGTTTTT TACTCGTCAT ATAAGAGAAA CGTCGATAAT	780
TTCAGATTCT TCTTGCGGAA TTATATGCCT TTGATATCTG ACGTCTTTGT CTTCCAGTGG	840
GTAAAACCCG CGCCGGATGT TCGGCTGCTT TTTGAGTTAA GTGCAGCGGA ACTAACGCTG	900
GAGGTTCCCA CACTGAGTTT GATAGATTCT CAAGTTGTGG TAGGTCATAT CTTAAGATAC	960
GTAGAATCCT ACACATCAGA TCCAGCCATC GACGCGTTAG AAGACAAACT GGAAGCGATA	1020
CTGAAAAGTA GCAATCCCCG TCTATCGACA GCGCAACTAT GGGTTGGTTT CTTTGTGTAC	1080
TATGGTGAGT TTCGTACGGC TCAAAGTAGA GTAGTGCAAA GACCAGGCGT ATACAAAACA	1140
CCTGACTCAG TGGGTGGATT TGAAATAAAC ATGAAAGATG TTGAGAAATT CTTGATAAAA	1200

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CTTCAGAGAG AATTGCCTAA TGTATCTTTG CGGCGTCAGT TTAACGGAGC TAGAGCGCAT 1260
 GAGGCTTTCA AAATATTTAA AAACGGAAAT ATAAGTTTCA GACCTATATC GCGTTTAAAC 1320
 GTGCCTAGAG AGTTCTGGTA TCTGAACATA GACTACTTCA GGCACGCGAA TAGGTCCGGG 1380
 TTAACCGAAG AAGAAATACT CATCCTAAAC AACATAAGCG TTGATGTTAG GAAGTTATGC 1440
 GCTGAGAGAG CGTGCAATAC CCTACCTAGC GCGAAGCGCT TTAGTAAAAA TCATAAGAGT 1500
 AATATACAAT CATCACGCCA AGAGCGGAGG ATTAAAGACC CATTGGTAGT CCTGAAAGAC 1560
 ACTTTATATG AGTTCCAACA CAAGCGTGCC GGTGTTTTGGT CTCGAAGCAC TCGAGACCTC 1620
 GGGAGTCGTG CTGACCACGC GAAAGGAAGC GGTGTA 1656

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Asn Tyr Ser Trp Glu Ser Leu Phe Lys Lys Phe Tyr Gly Glu
 1 5 10 15
 Ala Asp Trp Lys Lys Tyr Leu Ser Arg Ser Ile Ala Ala His Ser Ser
 20 25 30
 Glu Ile Lys Thr Leu Pro Asp Ile Arg Leu Tyr Gly Gly Arg Val Val
 35 40 45
 Lys Lys Ser Glu Phe Glu Ser Ala Leu Pro Asn Ser Phe Glu Gln Glu
 50 55 60
 Leu Gly Leu Phe Ile Leu Ser Glu Arg Glu Val Gly Trp Ser Lys Leu
 65 70 75 80
 Cys Gly Ile Thr Val Glu Glu Ala Ala Tyr Asp Leu Thr Asn Pro Lys
 85 90 95
 Ala Tyr Lys Phe Thr Ala Glu Thr Cys Ser Pro Asp Val Lys Gly Glu
 100 105 110
 Gly Gln Lys Tyr Ser Met Glu Asp Val Met Asn Phe Met Arg Leu Ser
 115 120 125
 Asn Leu Asp Val Asn Asp Lys Met Leu Thr Glu Gln Cys Trp Ser Leu
 130 135 140
 Ser Asn Ser Cys Gly Glu Leu Ile Asn Pro Asp Asp Lys Gly Arg Phe

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145		150		155		160									
Val	Ala	Leu	Thr	Phe	Lys	Asp	Arg	Asp	Thr	Ala	Asp	Asp	Thr	Gly	Ala
				165					170					175	
Ala	Asn	Val	Glu	Cys	Arg	Val	Gly	Asp	Tyr	Leu	Val	Tyr	Ala	Met	Ser
			180					185						190	
Leu	Phe	Glu	Gln	Arg	Thr	Gln	Lys	Ser	Gln	Ser	Gly	Asn	Ile	Ser	Leu
		195					200					205			
Tyr	Glu	Lys	Tyr	Cys	Glu	Tyr	Ile	Arg	Thr	Tyr	Leu	Gly	Ser	Thr	Asp
	210						215				220				
Leu	Phe	Phe	Thr	Ala	Pro	Asp	Arg	Ile	Pro	Leu	Leu	Thr	Gly	Ile	Leu
225					230					235					240
Tyr	Asp	Phe	Cys	Lys	Glu	Tyr	Asn	Val	Phe	Tyr	Ser	Ser	Tyr	Lys	Arg
			245						250					255	
Asn	Val	Asp	Asn	Phe	Arg	Phe	Phe	Leu	Ala	Asn	Tyr	Met	Pro	Leu	Ile
		260						265					270		
Ser	Asp	Val	Phe	Val	Phe	Gln	Trp	Val	Lys	Pro	Ala	Pro	Asp	Val	Arg
		275					280					285			
Leu	Leu	Phe	Glu	Leu	Ser	Ala	Ala	Glu	Leu	Thr	Leu	Glu	Val	Pro	Thr
	290					295					300				
Leu	Ser	Leu	Ile	Asp	Ser	Gln	Val	Val	Val	Gly	His	Ile	Leu	Arg	Tyr
305					310					315				320	
Val	Glu	Ser	Tyr	Thr	Ser	Asp	Pro	Ala	Ile	Asp	Ala	Leu	Glu	Asp	Lys
				325					330					335	
Leu	Glu	Ala	Ile	Leu	Lys	Ser	Ser	Asn	Pro	Arg	Leu	Ser	Thr	Ala	Gln
		340						345					350		
Leu	Trp	Val	Gly	Phe	Phe	Cys	Tyr	Tyr	Gly	Glu	Phe	Arg	Thr	Ala	Gln
	355					360						365			
Ser	Arg	Val	Val	Gln	Arg	Pro	Gly	Val	Tyr	Lys	Thr	Pro	Asp	Ser	Val
	370				375						380				
Gly	Gly	Phe	Glu	Ile	Asn	Met	Lys	Asp	Val	Glu	Lys	Phe	Phe	Asp	Lys
385					390					395					400
Leu	Gln	Arg	Glu	Leu	Pro	Asn	Val	Ser	Leu	Arg	Arg	Gln	Phe	Asn	Gly
			405					410					415		
Ala	Arg	Ala	His	Glu	Ala	Phe	Lys	Ile	Phe	Lys	Asn	Gly	Asn	Ile	Ser
		420						425					430		
Phe	Arg	Pro	Ile	Ser	Arg	Leu	Asn	Val	Pro	Arg	Glu	Phe	Trp	Tyr	Leu
	435					440						445			
Asn	Ile	Asp	Tyr	Phe	Arg	His	Ala	Asn	Arg	Ser	Gly	Leu	Thr	Glu	Glu

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450		455		460	
Glu Ile Leu Ile Leu Asn Asn Ile Ser Val Asp Val Arg Lys Leu Cys					
465		470		475	480
Ala Glu Arg Ala Cys Asn Thr Leu Pro Ser Ala Lys Arg Phe Ser Lys					
	485		490		495
Asn His Lys Ser Asn Ile Gln Ser Ser Arg Gln Glu Arg Arg Ile Lys					
	500		505		510
Asp Pro Leu Val Val Leu Lys Asp Thr Leu Tyr Glu Phe Gln His Lys					
	515		520		525
Arg Ala Gly Trp Gly Ser Arg Ser Thr Arg Asp Leu Gly Ser Arg Ala					
	530		535		540
Asp His Ala Lys Gly Ser Gly					
545		550			

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGTTCCA ACACAAGCGT GCCGGTTGGG GGTCTCGAAG CACTCGAGAC CTCGGGAGTC	60
GTGCTGACCA CGCGAAAGGA AGCGGTTGAT AAGTTTTTTTA ATGAACTAAA AAACGAAAAT	120
TACTCATCAG TTGACAGCAG CCGATTAAGC GATTTCGGAAG TAAAAGAAGT GTTAGAGAAA	180
AGTAAAGAAA GTTTCAAAAG CGAACTGGCC TCCACTGACG AGCACTTCGT CTACCACATT	240
ATATTTTTTCT TAATCCGATG TGCTAAGATA TCGACAAGTG AAAAGGTGAA GTACGTTGGT	300
AGTCATACGT ACGTGGTCGA CGGAAAAACG TACACCGTTC TTGACGCTTG GGTATTCAAC	360
ATGATGAAAA GTCTCACGAA GAAGTACAAA CGAGTGAATG GTCTGCGTGC GTTCTGTTGC	420
GCGTGCGAAG ATCTATATCT AACCGTCGCA CCAATAATGT CAGAACGCTT TAAGACTAAA	480
GCCGTAGGGA TGAAAGGTTT GCCTGTTGGA AAGGAATACT TAGGCGCCGA CTTTCTTTTCG	540
GGAAGTAGCA AACTGATGAG CGATCACGAC AGGGCGGTCT CCATCGTTGC AGCGAAAAAC	600
GCTGTGCATC GTAGCGCTTT CACGGGTGGG GAGAGAAAGA TAGTTAGTTT GTATGATCTA	660
GGGAGGTACT AA	672

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Ser Ser Asn Thr Ser Val Pro Val Gly Gly Leu Glu Ala Leu Glu
1           5           10           15

Thr Ser Gly Val Val Leu Thr Thr Arg Lys Glu Ala Val Asp Lys Phe
          20           25           30

Phe Asn Glu Leu Lys Asn Glu Asn Tyr Ser Ser Val Asp Ser Ser Arg
          35           40           45

Leu Ser Asp Ser Glu Val Lys Glu Val Leu Glu Lys Ser Lys Glu Ser
          50           55           60

Phe Lys Ser Glu Leu Ala Ser Thr Asp Glu His Phe Val Tyr His Ile
65           70           75           80

Ile Phe Phe Leu Ile Arg Cys Ala Lys Ile Ser Thr Ser Glu Lys Val
          85           90           95

Lys Tyr Val Gly Ser His Thr Tyr Val Val Asp Gly Lys Thr Tyr Thr
          100          105          110

Val Leu Asp Ala Trp Val Phe Asn Met Met Lys Ser Leu Thr Lys Lys
          115          120          125

Tyr Lys Arg Val Asn Gly Leu Arg Ala Phe Cys Cys Ala Cys Glu Asp
          130          135          140

Leu Tyr Leu Thr Val Ala Pro Ile Met Ser Glu Arg Phe Lys Thr Lys
145          150          155          160

Ala Val Gly Met Lys Gly Leu Pro Val Gly Lys Glu Tyr Leu Gly Ala
          165          170          175

Asp Phe Leu Ser Gly Thr Ser Lys Leu Met Ser Asp His Asp Arg Ala
          180          185          190

Val Ser Ile Val Ala Ala Lys Asn Ala Val Asp Arg Ser Ala Phe Thr
          195          200          205

Gly Gly Glu Arg Lys Ile Val Ser Leu Tyr Asp Leu Gly Arg Tyr
210          215          220

```

(2) INFORMATION FOR SEQ ID NO:14:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

ATGGAGTTGA TGTCCGACAG CAACCTTAGC AACCTGGTGA TAACCGACGC CTCTAGTCTA      60
AATGGTGTCG ACAAGAAGCT TTTATCTGCT GAAGTTGAAA AAATGTTGGT GCAGAAAGGG      120
GCTCCTAACG AGGGTATAGA AGTGGTGTTT GGTCTACTCC TTTACGCACT CGCGGCAAGA      180
ACCACGTCTC CTAAGGTTCA GCGCGCAGAT TCAGACGTTA TATTTTCAAA TAGTTTCGGA      240
GAGAGGAATG TGGTAGTAAC AGAGGGTGAC CTTAAGAAGG TACTCGACGG GTGTGCGCCT      300
CTCACTAGGT TACTAATAA ACTTAGAACG TTCGGTCGTA CTTTCACTGA GGCTTACGTT      360
GACTTTTGTA TCGCGTATAA GCACAAATTA CCCCAACTCA ACGCCGCGGC GGAATTGGGG      420
ATTCCAGCTG AAGATTCGTA CTTAGCTGCA GATTTTCTGG GTACTTGCCC GAAGCTCTCT      480
GAATTACAGC AAAGTAGGAA GATGTTCGCG AGTATGTACG CTCTAAAAAC TGAAGGTGGA      540
GTGGTAAATA CACCAGTGAG CAATCTGCGT CAGCTAGGTA GAAGGGAAGT TATGTAA      597

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Glu Leu Met Ser Asp Ser Asn Leu Ser Asn Leu Val Ile Thr Asp
1           5           10           15
Ala Ser Ser Leu Asn Gly Val Asp Lys Lys Leu Leu Ser Ala Glu Val
20           25           30
Glu Lys Met Leu Val Gln Lys Gly Ala Pro Asn Glu Gly Ile Glu Val
35           40           45
Val Phe Gly Leu Leu Leu Tyr Ala Leu Ala Ala Arg Thr Thr Ser Pro
50           55           60
Lys Val Gln Arg Ala Asp Ser Asp Val Ile Phe Ser Asn Ser Phe Gly

```

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65		70		75		80
Glu Arg Asn Val Val Val Thr Glu Gly Asp Leu Lys Lys Val Leu Asp						
	85			90		95
Gly Cys Ala Pro Leu Thr Arg Phe Thr Asn Lys Leu Arg Thr Phe Gly						
	100		105		110	
Arg Thr Phe Thr Glu Ala Tyr Val Asp Phe Cys Ile Ala Tyr Lys His						
	115		120		125	
Lys Leu Pro Gln Leu Asn Ala Ala Ala Glu Leu Gly Ile Pro Ala Glu						
	130		135		140	
Asp Ser Tyr Leu Ala Ala Asp Phe Leu Gly Thr Cys Pro Lys Leu Ser						
	145		150		155	160
Glu Leu Gln Gln Ser Arg Lys Met Phe Ala Ser Met Tyr Ala Leu Lys						
		165		170		175
Thr Glu Gly Gly Val Val Asn Thr Pro Val Ser Asn Leu Arg Gln Leu						
	180		185		190	
Gly Arg Arg Glu Val Met						
	195					

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGAAGATT ACGAAGAAAA ATCCGAATCG CTCATACTGC TACGCACGAA TCTGAACACT	60
ATGCTTTTAG TGGTCAAGTC CGATGCTAGT GTAGAGCTGC CTAAACTACT AATTGCGGT	120
TACTTACGAG TGTCAGGACG TGGGGAGGTG ACGTGTTGCA ACCGTGAGGA ATTAACAAGA	180
GATTTTGAGG GCAATCATCA TACGGTGATC CGTTCTAGAA TCATACAATA TGACAGCGAG	240
TCTGCTTTTG AGGAATTCAA CAACTCTGAT TGCCTAGTGA AGTTTTTCCT AGAGACTGGT	300
AGTGTCTTTT GGTTTTTCCT TCGAAGTGAA ACCAAAGGTA GAGCGGTGCG ACATTGCGC	360
ACCTTCTTCG AAGCTAACAA TTTCTTCTTT GGATCGCATT GCGGTACCAT GGAGTATTGT	420
TTGAAGCAGG TACTAACTGA AACTGAATCT ATAATCGATT CTTTTTGCGA AGAAAGAAAT	480
CGTTAA	486

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Glu Asp Tyr Glu Glu Lys Ser Glu Ser Leu Ile Leu Leu Arg Thr
1           5           10           15

Asn Leu Asn Thr Met Leu Leu Val Val Lys Ser Asp Ala Ser Val Glu
20           25           30

Leu Pro Lys Leu Leu Ile Cys Gly Tyr Leu Arg Val Ser Gly Arg Gly
35           40           45

Glu Val Thr Cys Cys Asn Arg Glu Glu Leu Thr Arg Asp Phe Glu Gly
50           55           60

Asn His His Thr Val Ile Arg Ser Arg Ile Ile Gln Tyr Asp Ser Glu
65           70           75           80

Ser Ala Phe Glu Glu Phe Asn Asn Ser Asp Cys Val Val Lys Phe Phe
85           90           95

Leu Glu Thr Gly Ser Val Phe Trp Phe Phe Leu Arg Ser Glu Thr Lys
100          105          110

Gly Arg Ala Val Arg His Leu Arg Thr Phe Phe Glu Ala Asn Asn Phe
115          120          125

Phe Phe Gly Ser His Cys Gly Thr Met Glu Tyr Cys Leu Lys Gln Val
130          135          140

Leu Thr Glu Thr Glu Ser Ile Ile Asp Ser Phe Cys Glu Glu Arg Asn
145          150          155          160

Arg

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

ATGAGGGTTA TAGTGTCTCC TTATGAAGCT GAAGACATTC TGAAAAGATC GACTGACATG      60
TTACGAAACA TAGACAGTGG GGTCTTGAGC ACTAAGAAT GTATCAAGGC ATTCTCGACG      120
ATAACGCGAG ACCTACATTG TGCGAAGGCT TCCTACCAGT GGGGTGTTGA CACTGGGTTA      180
TATCAGCGTA ATTGCGCTGA AAAACGTTTA ATTGACACGG TGGAGTCAAA CATACGGTTG      240
GCTCAACCTC TCGTGCGTGA AAAAGTGGCG GTTCATTTTT GTAAGGATGA ACCAAAAGAG      300
CTAGTAGCAT TCATCACGCG AAAGTACGTG GAACTCACGG GCGTGGGAGT GAGAGAAGCG      360
GTGAAGAGGG AAATGCGCTC TCTTACCAA ACAGTTTTAA ATAAATGTC TTTGGAAATG      420
GCGTTTTACA TGTCACCACG AGCGTGGAAA AACGCTGAAT GGTTAGAACT AAAATTTTCA      480
CCTGTGAAAA TCTTTAGAGA TCTGCTATTA GACGTGGAAA CGCTCAACGA ATTGTGCGCC      540
GAAGATGATG TTCACGTCGA CAAAGTAAAT GAGAATGGGG ACGAAAATCA CGACCTCGAA      600
CTCCAAGACG AATGTTAA                                     618

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Arg Val Ile Val Ser Pro Tyr Glu Ala Glu Asp Ile Leu Lys Arg
1           5           10           15
Ser Thr Asp Met Leu Arg Asn Ile Asp Ser Gly Val Leu Ser Thr Lys
20        25        30
Glu Cys Ile Lys Ala Phe Ser Thr Ile Thr Arg Asp Leu His Cys Ala
35        40        45
Lys Ala Ser Tyr Gln Trp Gly Val Asp Thr Gly Leu Tyr Gln Arg Asn
50        55        60
Cys Ala Glu Lys Arg Leu Ile Asp Thr Val Glu Ser Asn Ile Arg Leu
65        70        75        80
Ala Gln Pro Leu Val Arg Glu Lys Val Ala Val His Phe Cys Lys Asp
85        90        95
Glu Pro Lys Glu Leu Val Ala Phe Ile Thr Arg Lys Tyr Val Glu Leu
100       105       110

```

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Thr	Gly	Val	Gly	Val	Arg	Glu	Ala	Val	Lys	Arg	Glu	Met	Arg	Ser	Leu
	115						120					125			
Thr	Lys	Thr	Val	Leu	Asn	Lys	Met	Ser	Leu	Glu	Met	Ala	Phe	Tyr	Met
	130					135					140				
Ser	Pro	Arg	Ala	Trp	Lys	Asn	Ala	Glu	Trp	Leu	Glu	Leu	Lys	Phe	Ser
145					150					155					160
Pro	Val	Lys	Ile	Phe	Arg	Asp	Leu	Leu	Leu	Asp	Val	Glu	Thr	Leu	Asn
				165					170					175	
Glu	Leu	Cys	Ala	Glu	Asp	Asp	Val	His	Val	Asp	Lys	Val	Asn	Glu	Asn
			180					185					190		
Gly	Asp	Glu	Asn	His	Asp	Leu	Glu	Leu	Gln	Asp	Glu	Cys			
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGCTGGAGCT TGAGGTTCTG C

21

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGAATTCAC CATGGAGTTG ATGTCCGACA G

31

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCGGATCCA TGGCAGATTC GTGCGTAGCA GTA

33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACATTGGTTA AGTTTAACGA AAATGATTAG TAAATAATAA ATCGAACGTG GGTGTATCTA	60
CCTGACGTAT CAACTTAAGC TGTTACTGAG TAATTAAACC AACAAGTGTT GGTGTAATGT	120
GTATGTTGAT GTAGAGAAAA ATCCGTTTGT AGAACGGTGT TTTTCTCTTC TTTATTTTTA	180
AAAAAAAAAT AAAAAAAAAA AAAAAAAGC GGCCGC	216

WHAT IS CLAIMED:

1. An isolated protein or polypeptide corresponding to a protein or polypeptide of a grapevine leafroll virus (type 2).
2. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.
3. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is a polyprotein.
4. An isolated protein or polypeptide according to claim 3, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 3.
5. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is an RNA-dependent RNA polymerase having a molecular weight of from about 50 to about 54 kDa.
6. An isolated protein or polypeptide according to claim 5, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 5.
7. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is a heat shock 70 protein having a molecular weight of from about 63 to about 67 kDa.
8. An isolated protein or polypeptide according to claim 7, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 9.
9. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is a heat shock 90 protein having a molecular weight of from about 61 to about 65 kDa.

10. An isolated protein or polypeptide according to claim 9, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 11.

11. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is a coat protein having a molecular weight of from about 20 to about 24 kDa.

12. An isolated protein or polypeptide according to claim 11, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 15.

13. An isolated protein or polypeptide according to claim 2, wherein the protein or polypeptide is a diverged coat protein having a molecular weight of from about 23 to about 27 kDa.

14. An isolated protein or polypeptide according to claim 13, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 13.

15. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 7.

16. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 17.

17. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 19.

18. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide is purified.

19. An isolated protein or polypeptide according to claim 1, wherein the protein or polypeptide is recombinant.
20. An isolated RNA molecule encoding a protein or polypeptide according to claim 1.
21. An isolated RNA molecule according to claim 20, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.
22. An isolated DNA molecule encoding a protein or polypeptide according to claim 1.
23. An isolated DNA molecule according to claim 22, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.
24. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is a polyprotein comprising conserved regions of a helicase, a papain-like protease, and a methyltransferase.
25. An isolated DNA molecule according to claim 24, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 3.
26. An isolated DNA molecule according to claim 25, wherein the DNA molecule has a nucleotide sequence corresponding to SEQ. ID. No. 2.
27. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is an RNA-dependent RNA polymerase having a molecular weight of from about 50 to about 54 kDa.
28. An isolated DNA molecule according to claim 27, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 5.

29. An isolated DNA molecule according to claim 28, wherein the DNA molecule has a nucleotide sequence corresponding to SEQ. ID. No. 4.

30. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is a heat shock 70 protein having a molecular weight of from about 63 to about 67 kDa.

31. An isolated DNA molecule according to claim 30, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 9.

32. An isolated DNA molecule according to claim 31, wherein the DNA molecule has a nucleotide sequence corresponding to SEQ. ID. No. 8.

33. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is a heat shock 90 protein having a molecular weight of from about 61 to about 65 kDa.

34. An isolated DNA molecule according to claim 33, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 11.

35. An isolated DNA molecule according to claim 34, wherein the DNA molecule has a nucleotide sequence corresponding to SEQ. ID. No. 10.

36. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is a coat protein having a molecular weight of from about 20 to about 24 kDa.

37. An isolated DNA molecule according to claim 36, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 15.

38. An isolated DNA molecule according to claim 37, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 14.

39. An isolated DNA molecule according to claim 23, wherein the protein or polypeptide is a diverged coat protein having a molecular weight of from about 23 to about 27 kDa.

40. An isolated DNA molecule according to claim 39, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 13.

41. An isolated DNA molecule according to claim 40, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 12.

42. An isolated DNA molecule according to claim 22, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 7.

43. An isolated DNA molecule according to claim 42, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 6.

44. An isolated DNA molecule according to claim 22, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 17.

45. An isolated DNA molecule according to claim 44, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 16.

46. An isolated DNA molecule according to claim 22, wherein the protein or polypeptide comprises an amino acid sequence corresponding to SEQ. ID. No. 19.

47. An isolated DNA molecule according to claim 46, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 18.

48. An isolated DNA molecule according to claim 22, wherein the DNA molecule comprises a nucleotide sequence corresponding to SEQ. ID. No. 23.

49. An expression system comprising an DNA molecule according to claim 22 in a vector heterologous to the DNA molecule.

50. An expression system according to claim 49, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent

RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

51. A host cell transformed with a heterologous DNA molecule according to claim 22.

52. A host cell according to claim 51, wherein the host cell is selected from the group consisting of *Agrobacterium vitis* and *Agrobacterium tumefaciens*.

53. A host cell according to claim 51, wherein the host cell is selected from a group consisting of a grape cell, a citrus cell, a beet cell, and a tobacco cell.

54. A host cell according to claim 51, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

55. A transgenic plant cultivar comprising the DNA molecule according to claim 22.

56. A transgenic plant cultivar according to claim 55, wherein the plant cultivar is selected from a group consisting of a grape plant cultivar, a citrus plant cultivar, a beet plant cultivar, and a tobacco plant cultivar.

57. A transgenic plant cultivar according to claim 55, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

58. A method of imparting grapevine leafroll virus resistance to a *Vitis* scion or rootstock cultivar or a *Nicotiana* cultivar comprising:

transforming a *Vitis* scion or rootstock cultivar or a *Nicotiana* cultivar with a DNA molecule according to claim 22.

59. A method according to claim 58, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA

polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

60. A method according to claim 58, wherein the grapevine leafroll virus is GLRaV-2.

61. A method according to claim 58, wherein said transforming is *Agrobacterium* mediated.

62. A method according to claim 58, wherein said transforming comprises:
propelling particles at grape or tobacco plant cells under conditions effective for the particles to penetrate into the cell interior and
introducing an expression vector comprising the DNA molecule into the cell interior.

63. A method of imparting beet yellows virus resistance to a beet cultivar comprising:
transforming a beet cultivar with a DNA molecule according to claim 22.

64. A method according to claim 63, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

65. A method according to claim 63, wherein said transforming is *Agrobacterium* mediated.

66. A method according to claim 63, wherein said transforming comprises:
propelling particles at beet plant cells under conditions effective for the particles to penetrate into the cell interior and
introducing an expression vector comprising the DNA molecule into the cell interior.

67. A method of imparting tristeza virus resistance to a citrus scion cultivar or rootstock cultivar comprising:

radioimmunoassay, gel diffusion precipitin reaction assay, immunodiffusion assay, agglutination assay, fluorescent immunoassay, protein A immunoassay, and immunoelectrophoresis assay.

75. A method for detection of grapevine leafroll virus in a sample, said method comprising:

providing a nucleotide sequence of the DNA molecule according to claim 22 as a probe in a nucleic acid hybridization assay;

contacting the sample with the probe; and

detecting any reaction which indicates that grapevine leafroll virus is present in the sample.

76. A method according to claim 75, wherein the nucleic acid hybridization assay is selected from a group consisting of dot blot hybridization, tissue printing, southern hybridization, and northern hybridization.

77. A method for detection of grapevine leafroll virus in a sample:

providing a nucleotide sequence of the DNA molecule according to claim 22 as a probe in a gene amplification detection procedure;

contacting the sample with the probe; and

detecting any reaction which indicates that grapevine leafroll virus is present in the sample.

78. A method according to claim 77, wherein the gene amplification detection procedure is selected from a group consisting of polymerase chain reaction and immunocapture polymerase chain reaction.

transforming a citrus scion cultivar or rootstock cultivar with a DNA molecule according to claim 22.

68. A method according to claim 67, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

69. A method according to claim 67, wherein said transforming is *Agrobacterium* mediated.

70. A method according to claim 67, wherein said transforming comprises: propelling particles at citrus plant cells under conditions effective for the particles to penetrate into the cell interior and introducing an expression vector comprising the DNA molecule into the cell interior.

71. An antibody or binding portion thereof or probe recognizing the protein or polypeptide according to claim 1.

72. An antibody or binding portion thereof or probe according to claim 71, wherein the protein or polypeptide is selected from a group consisting of a polyprotein, an RNA-dependent RNA polymerase, a heat shock 70 protein, a heat shock 90 protein, a diverged coat protein, and a coat protein.

73. A method for detection of grapevine leafroll virus in a sample, said method comprising:
providing an antibody or binding portion thereof recognizing the protein or polypeptide according to claim 1;
contacting the sample with the antibody or binding portion thereof; and
detecting any reaction which indicates that grapevine leafroll virus is present in the sample using an assay system.

74. A method according to claim 73, wherein the assay system is selected from a group consisting of enzyme-linked immunoabsorbent assay,

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FIG. 1A

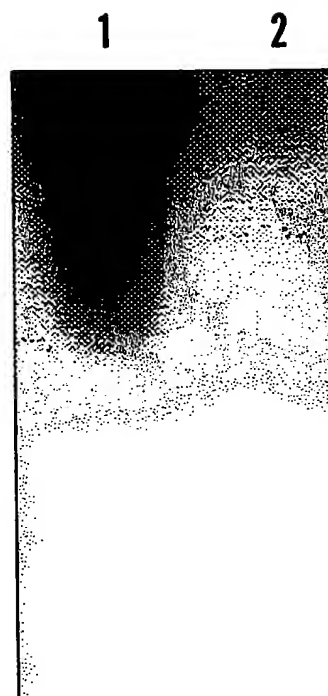


FIG. 1B

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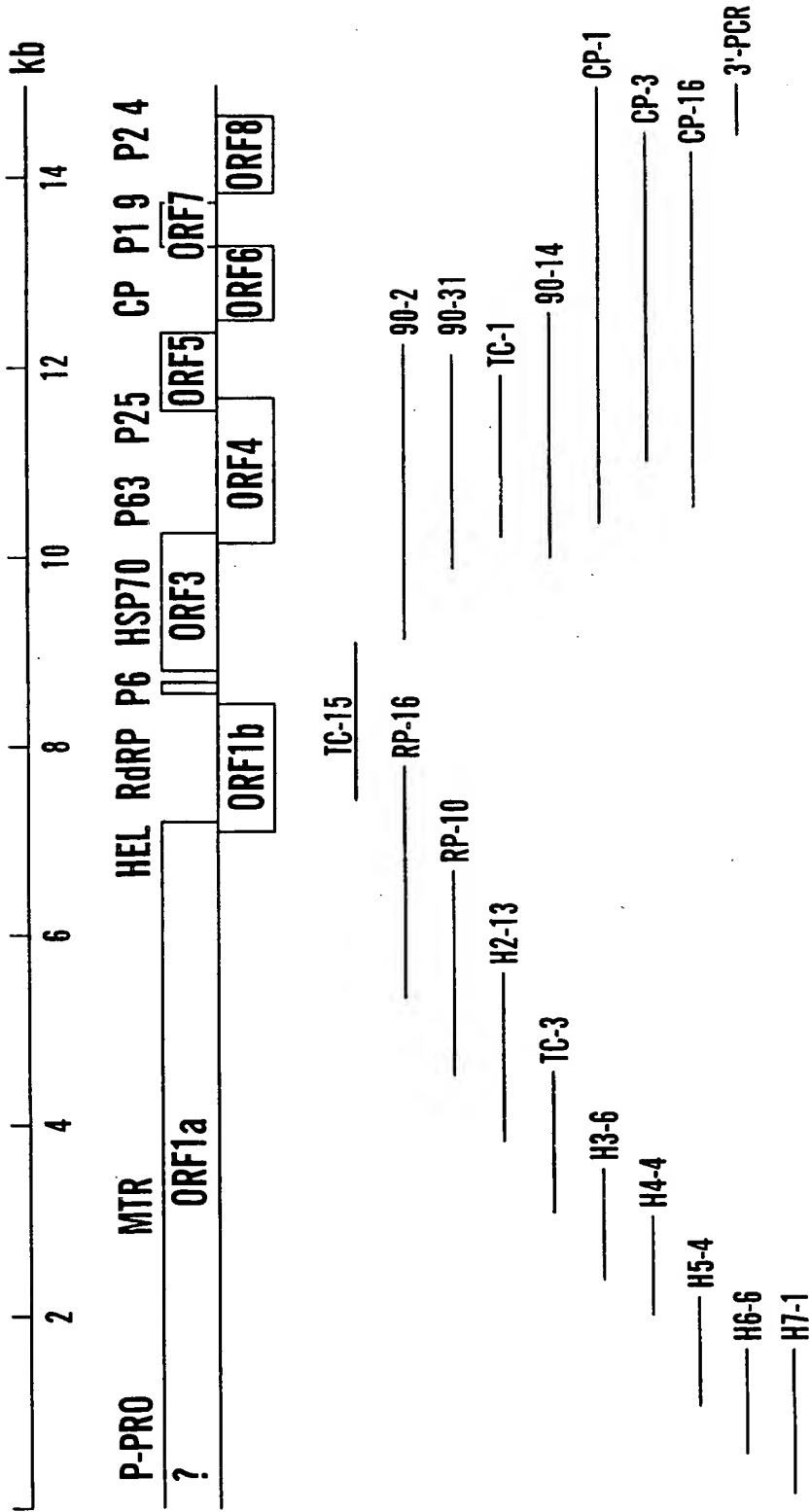


FIG. 2

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GLRaV2-PRO₁ SRVIYPDGRCYLAHMYLCAFYCRPFRESYALGMWPTVARLRACVEKNFGVEACGIALRGYITSRNVYHCDYDSAYVKYFRNLSSGRIG/G
 GLRaV2-PRO₂ TRIRYPNGFCYLAHCRYACAFLLRGFDPKRFDIGAPPTAAKLRNRMVSELGERSLGLNLYGAYTSRGVFHCDYDAKFIDKDLRLMSAVIA/G
 BYV-P-PRO LQYRPGEGLCYLAHAALCCALQKRTFREEDFFVGMPTKVFVAKRLTEKLGPSALKHPVRGRQVSRSLFHCDDVASAFSSPFYSLPRFIG/G
 ConsensusG.CYLAH....CA...R.F.....G..PT.....G.....G...SR...HCD.....I../G

FIG. 3A

MT I MT Ia MT II
 GLRaV2-MTR MSEATQNSLTRFYQPPELKFSSSHSDHPAAAAARLLENETLVRLCGNSVSDIGGCPLFHLHSTQRRVHVCPRVLDGKDAQRRVVRDLQ
 BYV-MTR MGEAVQSGLTRAYPQFNLSPTHSVSDHPAAAGSRLLNETLMAKSSFSDIGGCPLFHIK-RGSTDYHVCRIPYDMKDAQRRVSRELQ
 MT IIa MT III
 GLRaV2-MTR YSNVRLG-DDDKILEGPRNIDICHYPLGACDHESAMMMQVYDASLYEICGAMIKKSRITYLTMTVPGEPLDGRECVYMESLDCEIEV
 BYV-MTR ARGLVENLSREQVLEAQRVSVCPTLGNCCNVKSDVLIMQVYDASLNEIASAMVLKESKVAYLTMTVPGEPLDEREAFIDAIGCDVGVV
 MT IV
 GLRaV2-MTR DVHADVVMYKFGSSCYSHKLSIIKDINTTPYLTGGLFVSVMYEVRMGVNYFKITKSEVSPSISCTKLLRYRRANSDDVVKVLPFRD
 BYV-MTR DTRDMVQYKFGSSCYCHKLSNIKSIMLTAPFTSGNLFVSVMYENRMGVNYKITRSAYSPEIRGVKTLRYRRACTEVVQVKLPFRD

FIG. 3B

HEL I HEL Ia
 GLRaV2-Hel FVFTNSSVDILLYEAPPGGKTTTLIDSFLKVFKEVSTMLTANKSSQVEILKKVEKVSNIQCKRKDKRSPKKSIIYTDAYLMHHR
 BYV-Hel FTFTNLSANVLLYEAPPGGKTTTLIKVFCETFSK--VNSLILTANKSSREEILAKVNRIVLD-EGDTPLQTRDR---ILTIDSYLMNNR
 HEL II HEL III HEL IV
 GLRaV2-Hel GCDADVLFIDEC FMVHAGSVLACIEFTRCHKVMIFGDSRQIHYIERNELDKLYGDLDRFVLDQCRVYGNISYRCFWDVCAWLSTVYGNL
 BYV-Hel GLTCKVLYLDEC FMVHAGAAVACIEFTKCDASAILFGDSRQIRYGRCELDTAVLSDLNRFVDDSRVYGEVSYRCFWDVCAWLSTFYPKT
 HEL V
 GLRaV2-Hel IATVKGESEGGSSMRINEINSVDDLVPDVGSTFLCMLQSEKLEISKHF---IRKGLTKLNVLTVHEAQGETYARVNLVRLKFQEDPEPKS
 BYV-Hel VATTNLVSAGQSSMQVREIESVDDVEYSSEFVYLTMLQSEKDLLKSFGRSRSSVEKPTVLTVHEAQGETYRKVNLRVTKFQEDDPFRS
 HEL VI
 GLRaV2-Hel IRHITVALSRHTDSLTYNVLAARRGDATCDAIQAAELVNKFRVFTSFGGS
 BYV-Hel ENHITVALSRHVESLTYSVLSSKRDDAIAQAIKAKQLVDAYRVYFTSFGGS

FIG. 3C

RdRP I RdRP II RdRP III
 GLRaV2-RdRP ICRFKLMVKRDAKVKLDSSCLTKHSAQNIMFHRKSINAIFSPIFNEVKNRIMCCLKPNIKFFTEMTNRDFASVVSNNLGDDEVDVHIGEV
 BYV-RdRP ITTFKLMVKRDAKVKLDSSCLVKHPPAQNIMFHRKAVNAIFSPCFDEFKNRVITCTNSNIVFFTEMTNSTLASIAKEMLGSEHVYNVGEI
 RdRP IV RdRP V
 GLRaV2-RdRP DFSKYDKSQDAFVKAEEVMYKELGVDEELLAIWMCGERLSIANTLDGQLSFTIENQRKSGASNTWIGNSLVTGLGILSLYDVVRNFEALY
 BYV-RdRP DFSKFDKSQDAF IKSFERTLYSAFGFDEDLDDVMMQGEYTSNATTLDGQLSFSVDNQRKSGASNTWIGNSIETGLGILSMFYTTNRFKALF
 RdRP VI RdRP VII RdRP VIII
 GLRaV2-RdRP ISGDDSLIFSRSEISNYADDICTDMGFETKFMSPSVPYFCSKFFVMCGHKTFFVDPYKLVKLGAVKEDVSMDFLFETFTSFKDLTSDF
 BYV-RdRP VSGDDSLIFSESPIRNSADAMCTELGFETKFLTPSVPYFCSKFFVMTGHDVFFVDPYKLVKLGASKDEVDDFLFEVFTSFRDLTKDL
 GLRaV2-RdRP NDERLIQKLAELVALKYEVQGTGNTTLAL
 BYV-RdRP VDERVIELLTHLVHISKYGYESGDTYAAAL

FIG. 3D
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GLRaV-2	CAUGAUAAGCAGOGUGUU <u>UAGCG</u> UAGUUCGGUCCAGGCGAUUCCGGUAGA
BYV	CACGACCCGCGAGGGGUU <u>UAGCT</u> OGAUUCGCUCCAGGCGAUUCCUAAGAGG
BYSV	CACGAUGAACAGCGGUGU <u>UAGCG</u> UAGUAGGUCCAGGCCAUCCUAAAAGG
CTV	CACGAACCGGCUCCGGU <u>UCCGG</u> UAGUAAGGUCACAAGCAUCCUCCAAGA
Consensus	CA.GA.....CG.GUU..GC....U....UC.CA.GC.AU.CC....AG.

FIG. 4A

GLRaV-2	H D K Q R V <u>S</u> V V R S Q A I P R R
BYV	H D P Q R V <u>S</u> S I R S Q A I P K R
BYSV	H D E Q R V <u>S</u> V V R S Q A I P K R
CTV	H E P A R V <u>G</u> V V R S Q A I P P R
Consensus	H . . . R V . . . R S Q A I P . R

FIG. 4B

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GLRaV2-HSP70	<u>A</u>	MVFGLDGTFSTVGVKDRVSEFQNSAVPTVLYLFDSDNMFGEAEIASMLKXGSEFYRLKRWGODSSNLDAVIDRLKP
BVH-HSP70		MVFGLDGTFSTVGVKDRVSEFQNSAVPTVLYLFDSDNMFGEAEIASMLKXGSEFYRLKRWGODSSNLDAVIDRLKP
GLRaV2-HSP70		<u>B</u>
BVH-HSP70		HYSVRLVKIGSGIAGNETIVSIGNFGGVKSEAHFGLJALFTKAVTSCAGAFACITCTGTCV/PANVDSVQRFIDQCVSLSGVCQVMTN
	<u>C</u>	<u>D</u>
GLRaV2-HSP70		EPSAALSAQNSIGKGSANLAVYDFCGGTFDSLSLSTANNFWRASGEANLGGVDVRAFLUHLFSLTSLSEPLTLDISNLKESLSKT
BVH-HSP70		EPSAALSAQNSIGKGSANLAVYDFCGGTFDSLSLSTANNFWRASGEANLGGVDVRAFLUHLFSLTSLSEPLTLDISNLKESLSKT
GLRaV2-HSP70		<u>E</u>
BVH-HSP70		DAEIVYILRGVDCRKEVVRNNILTSVLPVNRITKILKSTLKSZAKSNESARVKCDLWLGSSSYLPGLADVLTKHQSVDRILRVS
	<u>F</u>	<u>G</u>
GLRaV2-HSP70		DPRAAVAGGCALYSSCLSGGGLLITDCAHTVAIAIRSCHQILICAPAGAPIPFSGSMPLYLARVNNISQREVAVFEGEYVCEKPRKTC
BVH-HSP70		DARAAGGCALYSACLRNDSEMLLVDCAHNLSSKVCESIVCPAGSPIPTIGVIRVNMTCNBSAVYSAALFEGJFVKRLNKRIF
GLRaV2-HSP70		<u>H</u>
BVH-HSP70		GANIRFFDIGVTGDSYAPVTFYMDFSISSGVANSEVWRGPEKQVSLTGTTPANFSSVALGSRSVREHISIANKVFLGLJLHRAQDRRI
		FEDWLGNVGTSAIRIVPLTLEINVSIGTISFLVGTGVKLLGGVAYDFSSYQLGERVADLHKHNSDKVKLJLHALTYQFQRK
GLRaV2-HSP70		LFTKDEAIRVADSI--DIADVLRKYSAAALPPEDVEILLGKSVQVLRGSRLEEIPL.
BVH-HSP70		KLJDCXKALFLKRLTADYRRERKFFSSYDDNL---NSSELLGFLIIPKILRGSRVEKLD-V

FIG. 5

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GERA2-CP M-----ELNDN-----L-----SULVTD-----ASSIAGVKKLLSAEVRMLVK--GARNE
GERA2-CPd M--SSNTSVFVGELEALETSGWLTR--KEAVDF-----FNEIKENYSVDSRLSDSEVKELKSESEK--SELASTDE
BW-CP MOSEAP-----ISA-----IATFENSLAD-----QICLHEDDOCKLRNFEBCIKLK--GVFED
BW-CRd MLAPERGLIH-----FTENVRDMEIF-----FNSYLAESVNRKRNKREIDELGVTRERFK--SELATIDE
BISV-CP MAGND-----EGSDSSAQJMTND-----MIFAFENFARAS-----ATCINGENKKLFEBSVRVKIQ--DYTES
BISV-CRd M-PPQPCGAELVBNANKSSLEVFSSSEIREKVKF-----FNFEDHTEKQVNRNLLNEDELREVLCKLKEIK--TNLXALDE
CIV-CP MDEIKKLNKKEIKGGDWAESSFSSW-----LHDP--TLITND-----VRQSTQQAALNRULFLITLKEKHNLPIK
CIV-CRd M-AGTVLTKTDKENDFVSAVRGKVPDVIKFNARSVDALIBG/ISKLDNSIVDESTEFTGSHKXVVMVMDIFLL--ENYKIKTE
Consensus M.....S.....N..R.....

GERA2-CP GLEVFGLLVALARTSEKVRQRAEDVFESSEGE--RNWVTEBDLKKVLDSCAPLTF--TNKLRTGRTTEAYVDFC--IAVKHLRL
GERA2-CPd HFVYHI--IFEL--IRCANKUSTSEKVKY--AGSH--TWWDKTYVILDWVENWMSLTKKVRVAGLRAFC--CACEILYLIVA--PTMSERFKI--
BW-CP N/GIALGLCYSCNTIGTSNKVWQPTSIFKASFGCKELMTHSEIASFLSCQLLEKPNKLRCCKRIFQKQYISIRKVRGKLPFI
BW-CRd IFVKHLAFALIRANITVTSKWKY--AGAV--EVTIGCKRELWKDWVFLKECKKFNKPNVRKFCNTEFDAYIVTRPSLPKLFIN--
BISV-CP GEPITLGMVALATLSTSKIDIEKTPHNSAKIDAN--VITYEDIRNFASLTLKXVKNKLKVRKRTFESEYLRVQKXHLNFI
BISV-CRd IITYHVAFFELIRASWSTSEKVEY--HGSY--SVSTDRTKTVNDWIFPQKILASKHKNLRAFCASLEGMVLSVARUCPDFAFGI--
CIV-CP IKDERLAWMLVRLAVKSSSQSDDANGITYTR--HVEVLSDKMDVWNSKIGRITVALRWGRNDALYLAFCRQKRN--LSIG
CIV-CRd ILIWLMTIQKRLYITLSTSIKTKFRDKGCI--SWQGLRKVLIDKAVFPFLISKTFDRET--PALRKFACTFEELHLOARLPPILYEN--
ConsensusS.....N..R.....

GERA2-CP NPANELGIPADTSYLAADFL--GTCKKLSLEQQSRKMFASMAIKTEGGWNTP--VSNLRQLGRR--EVM
GERA2-CPd KAVGKKGLPVCKEYLCADFLSGTSCDMSDHRANSVIANKNAVIPSFAFTGGERKIVSLYDLGR--Y
BW-CP APANRHGLPABTHYLAADFT--STSTELDLQSR--ILLARENAVTHIEFSSES--P-VISLKQLGRELGTGR
BW-CRd RTTGRGIPSGVEFLCADFLJATSVCLNDEKATVLAQASRAAIDRAVSSSVGCKVSLFIDLGR--S
BISV-CP APANKHGPADYSYLAADFV--QT--SNLLKEHQAV--LLBERNAVATSSGITRES--ANNILKYLG--CS--SK
BISV-CRd RSVGRRGAPSGSEYLCADFLSTCFDMSDHRANVASRAALDPSAAQIDKXWLSYDFGKAWYT
CIV-CP GRPILDRGIPAGHYLCADFL--TGAGLTDE--CNVYQAKQQLKRRGADVV--VINVRQLGKE--NTR
CIV-CRd KRTTRAGTPEHKGYSADFLSGSLFGTSBERGILIPASEVILARQGYEEATELLNLRDLGK--YL
ConsensusG.P.....L.ADF.....G.....

FIG. 6A

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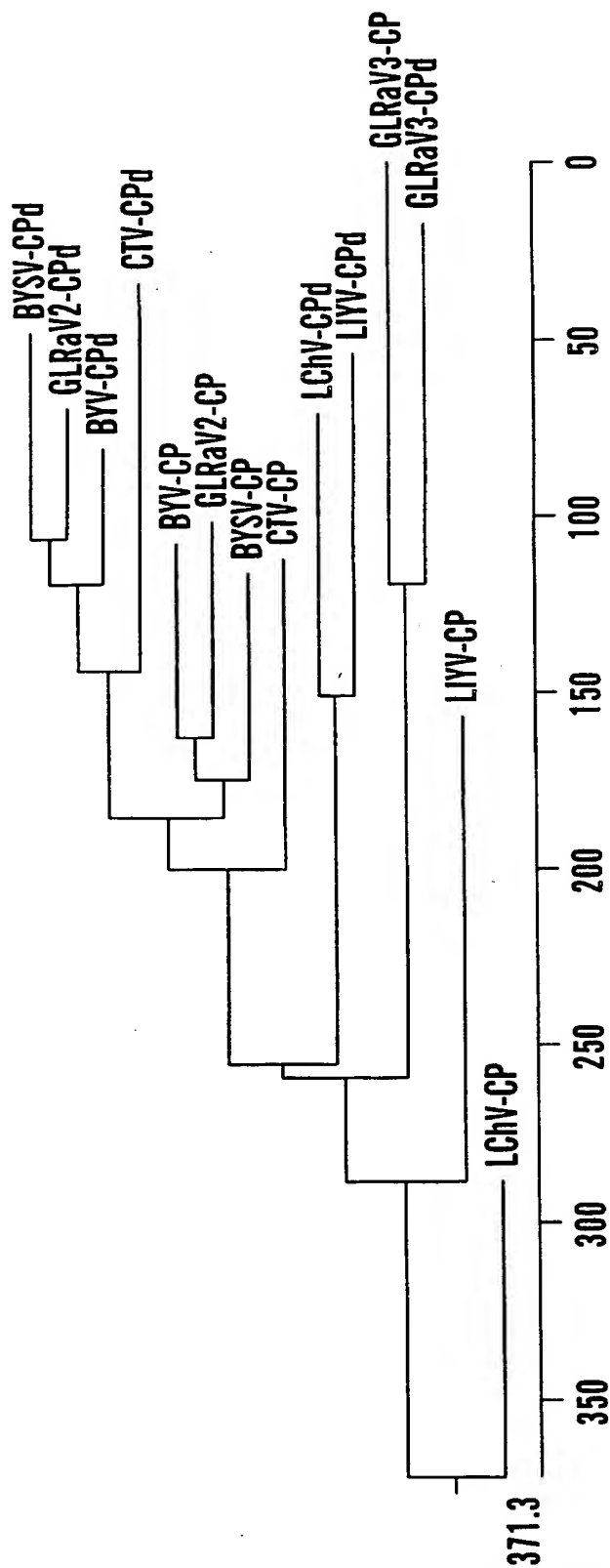


FIG. 6B

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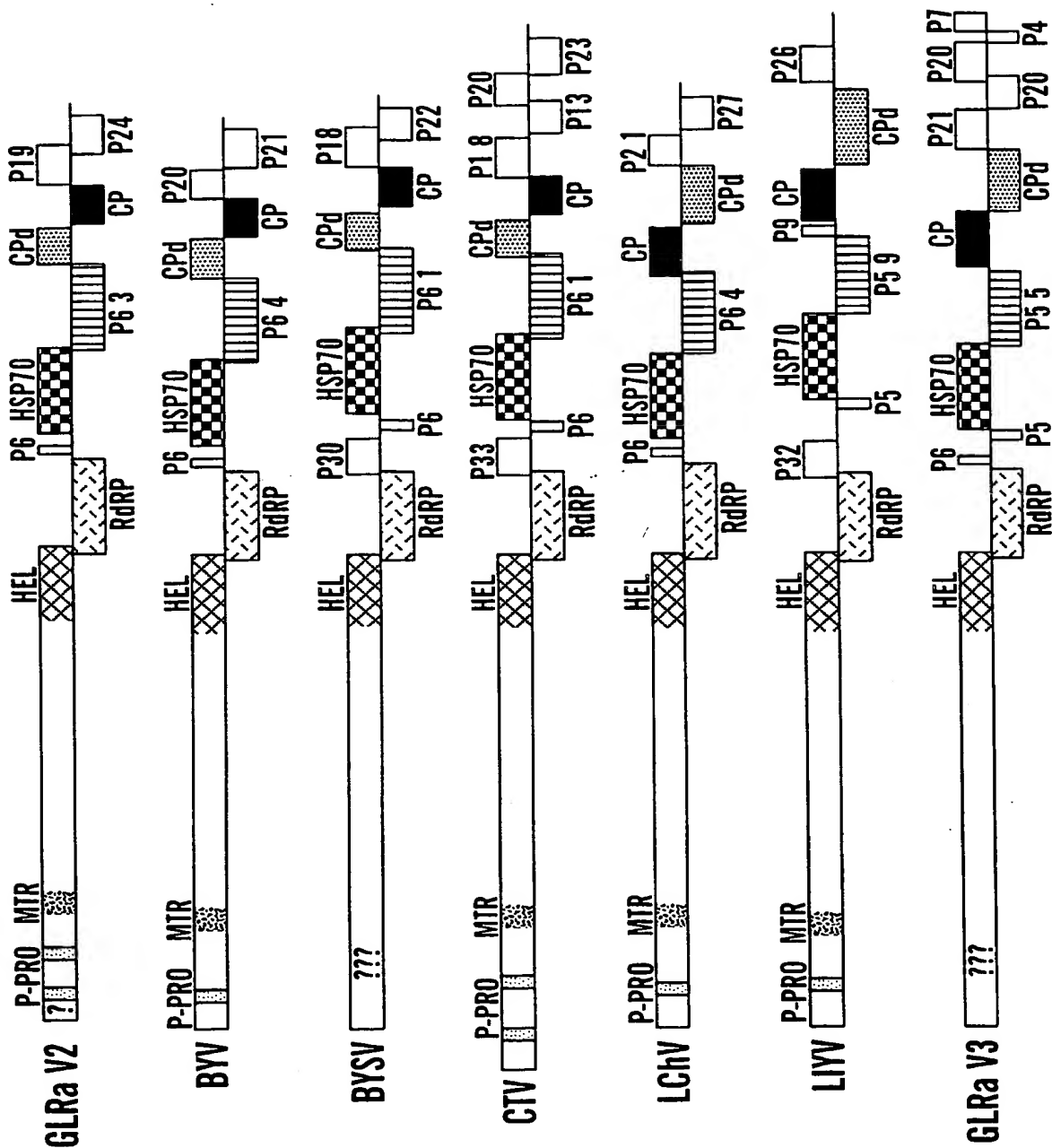
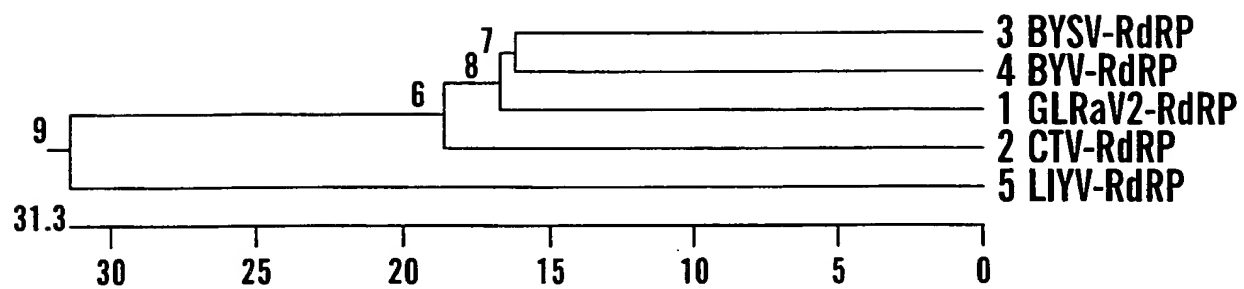


FIG. 7

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**FIG. 8**

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FIG. 9

GLRaV2-HSp90 MS-----NYSWESLFKKFYGEADWKYLSRSIAAHSSEIKTLPDIRLYGGRVVKSEFESALP
 BYV-HSP90 MTTRFSTPANYYWGELFRFRFGQEWKNLMSEAAVSRRPYSS--DFRFSGDVILSRKTFGESTG
 BYSV-HSP90 MSRR-PTFAGYSWGSFLFKRHYGEPEWKSYLETETSMKYPLKSE--SITFYDGSSLTSAELRPARS
 CTV-HSP90 MSSH-----HVWGSFLFRKFYGEAIWKEYLSESTRNFDERNVSL-DHTLSSGVVVRQSLNAPQ
 Consensus M.....W..LF...G...WK.....G.....

GLRaV2-HSp90 NSFEQE--LGLFILSEREVGWS-KLCGITVEEAAYDLTNPKAYKFTAETCSPDVKGEGQKYSMED
 BYV-HSP90 ESFVREFSL-LLTFPKTYE--VCKLCGVAMELALNGMNRSDYN-VSEFNIVDVKTGCKFNISQ
 BYSV-HSP90 GT--AEYEIALLI FSDSITKWSEKL-ERSIYRGLNQINNHSIYA-ETELEVTDVKTIGCKFTISA
 CTV-HSP90 GTFENE--LALLYNSVINDFVE-LTGMPLKSLMTGIEDRKV---PDELISVDPHEVGCRFTLND
 ConsensusE...L.....L.....E...D...G.....

GLRaV2-HSp90 VMNFMRLSNLDVNDKMLTEQCWSLSNSCGELINPDDKGRFVALTFKDRDTADDTGAANVECRVGD
 BYV-HSP90 VTEFVKKINGNVAEPSLVEHCWSLSNSCGELINPKDTKRFVSLIFKGDLAESTDEAIVSSSYLD
 BYSV-HSP90 VESFM----GGRASAAQVEHCWSLSNSCGELINPNDTARFIQLVFKDKAVTEQAQ-VNTSGSVSD
 CTV-HSP90 VESYLMSRGEDFADLAAVEHSWCLSNCGRLSSTEIDAYKTLVFT-KNF--DSNVSGVTTKLET
 Consensus V.....E..W.LSNSCG.L.....L.F.....

GLRaV2-HSp90 YLVYAMSLFEQRTQKSQSGNISLYEKEYCEYIRTYLGSTDLFFTAPDRIPLLTGILYDFCKEYNVF
 BYV-HSP90 YLSHCLNLYETCNLSSNSGKSLYDEFLKHVIDYLENSDLEYRSPDNPLVAGILYDMCFEYNTL
 BYSV-HSP90 YLVYCLQLYDNSKKKSNAGRTQLMESYVSFIRDFQHSDLYYRSPLDNPLLTGVLYDLCEIHNVL
 CTV-HSP90 YLSYCSISLYKKHCKMKDD-DYFNILIPMFNCLMKVLASGLFYEKHADNPLLTGMLIEFCLENKVY
 Consensus YL.....L.....L.....L.....PL..G.L...

GLRaV2-HSp90 YSSYKRNVDNFRFFLANYMPLISDVVFQWVKPAPDV----RLLFELSAEALTLEVPTLSLIDSQ
 BYV-HSP90 KSTYLKNIESFDCFLSLYLPLLSEVFSMNWERPAPDV----RLLFELDAAELLKLVPTINMHDST
 BYSV-HSP90 RGSYLKNLDNFRFLFKQTYLPMIDDIFDYSWELYAPDE----RLLFPIDPYEIIKEVPTMSVIDAN
 CTV-HSP90 YSTFKVNLNDNVRFLFKSKVLPVVLTV---WDISEPDDPMDERVLIPFDPTDFVLDLPKLNIDHTM
 ConsensusN.....F.....P.....W....PD.....R.L.....P.....D..

GLRaV2-HSp90 VVVGHIILRYVESYTSDDPAIDALEDKLEAILKSSNPRLSTAQLWVGFFCYGFEFRTAQSRVVQRP
 BYV-HSP90 FLYKNKLRYLESYFEDDSNELIKVKVDSLRLTRDNPELKLQAQRWVGFFHCYGVFRTAQTRKVKRDA
 BYSV-HSP90 VVLSNKLVLVLDSDYLENNISILALEKKIISILCRDNEGIDEGALWAAFFCYGTYRTARQVRVVRPD
 CTV-HSP90 VVVGNIQIRQLEYVVEDALDDLQSHVDLRLAADNPDLRVGLRWAGMFVYGVYRCVVDRAVERPT
 ConsensusL...N.....W.....YYG...R....R.V.R..

GLRaV2-HSp90 VYKTPDSV-----GGFEINMKDVEKFFDKLQRELPNVSLRRQFNGARAHEAFKIFKNGNISFRP
 BYV-HSP90 EYKLPPAL-----GEFVINMSGVEEFFEELQKMPISVRRRRCGSLSHEAFSVFKRFGVGFP
 BYSV-HSP90 TYELDGIF-----SKPIV-MSGVELFFDELQKRPVDSLRRRFNGAKAGEAITVFKKLGISFPP
 CTV-HSP90 LFRLPQKLLSQDDGESCSLHMGSVEALFNLVQKVNKDINVRQFMGRHSEVALRLRYNLGLRFPP
 ConsensusM..VE..F...Q.....RR.F.G....A.....F.P

GLRaV2-HSp90 ISRLNVPREFWYLNIDYFRHANRSGLTEEEILILNNISVDVRKLCAERACN-----TLPSAKR
 BYV-HSP90 ITRLNVPVKYSYLNVDYRHRVQRVGLTQDELTILSNIEFDVAEMCCEREVALQAR--RAQRGEKP
 BYSV-HSP90 ITRLNAPSKYSYLNIDYFKQANSGLTEPEKIIILCNIAKDVMCAQRISVKA-----KP
 CTV-HSP90 ISSVRLPAHHGYLYVDFYKRVDPGAVTADELESLRQLRSSVDVMCKDRVSITPPFPNRLRRGSSR
 Consensus I.....P....YL..D.....T..E...L.....V...C..R.....

GLRaV2-HSp90 FSKNHKSNIQSSRQERRIKDPLVVLKDTLYEFQHKRAGWGSRSRTRDLGSRADHAKGSG.
 BYV-HSP90 FQGWKGTKNEISPHARSSIRVKKNDSLLNWKDVGARSQRRLNPLHRK-----H
 BYSV-HSP90 IAQRNG--EAINSAKIRTLPTNTLVRALEKCLLNQAPSWWNTLTNL
 CTV-HSP90 TFRGRGARGASSRHSRDVATSGFNLPYHGRLY-----STS
 Consensus

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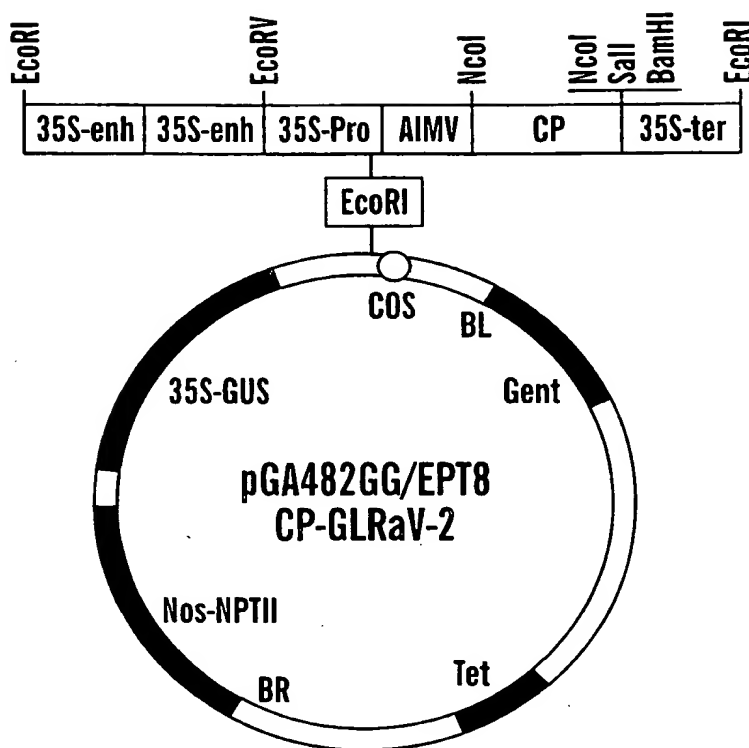
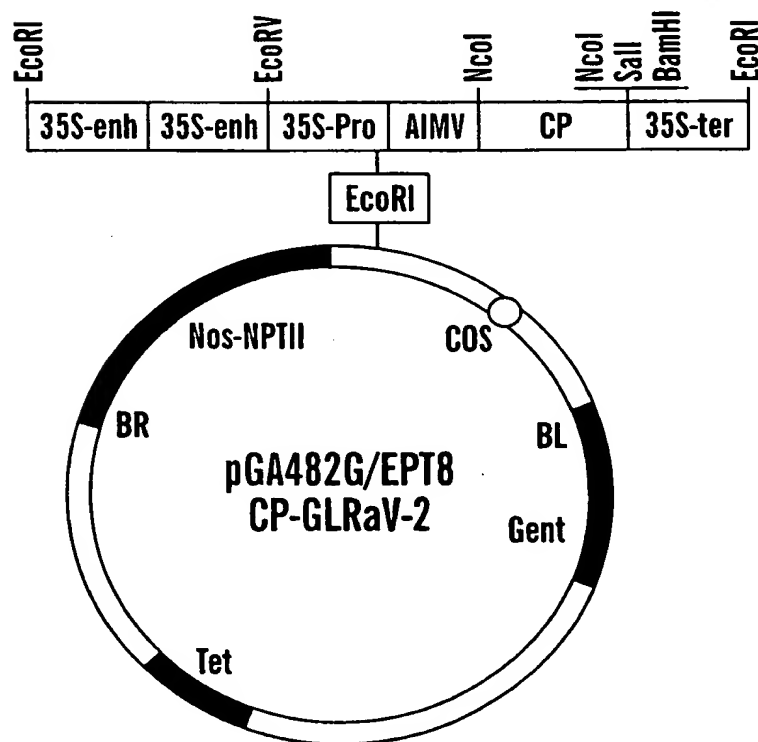
11/15

GLRaV2 3'-UTR	TTAAGCTGTTACTGAGTAATTAAACCAACCAAGTGTGGTGAATGTGTATGTGTATGTGTAGT	135
BYS 3'-UTR	TTAAGTCGTCACAGAGTGACAACGGCACCAAGTGGTGTAGTGGCGTATGTAAATTACGAA	95
BYSV 3'-UTR	TTAAGCCCTCACAGAGCGGAGAACGTTGGCAAGAGCCCAATTAGTGTGTGTGTAGTATAATTA	181
CTV 3'-UTR	CTAAGCTCCACAGAGTGGTAGTGGTCTCAAGTGAGGCTTAACGTTATCGGTGAACCAAGA	208
Consensus	.TAAG.....AC.GAG.....CAAG.G....T.....A	

FIG. 10

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**FIG. 11A****FIG. 11B**
SUBSTITUTE SHEET (RULE 26)

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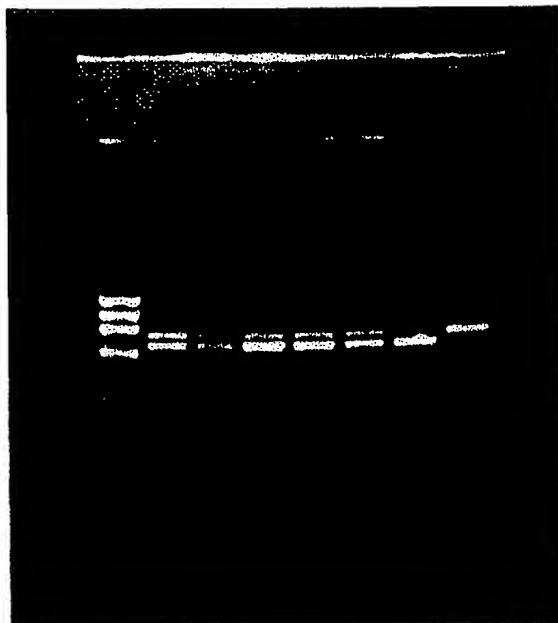


FIG. 12

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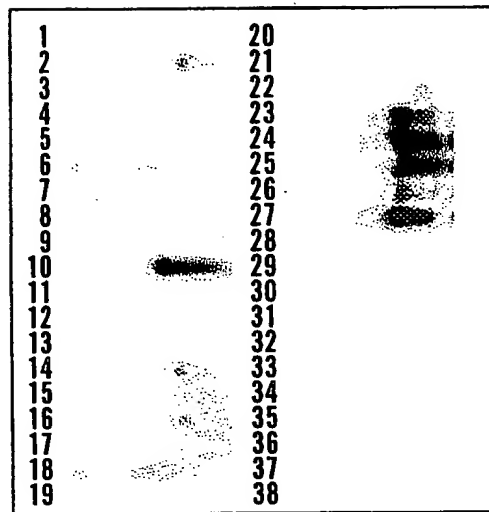
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FIG. 13

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**FIG. 14**

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10313

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/2, 44; 530/350, 826; 536/22.1, 23.72; 424/130.1, 159.1; 435/ 172.2, 172.3, 410; 436/512

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN, APS

search terms: protein, grapevine leafroll virus, tristeza virus, citrus plants

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 97/22700 A3 (CORNELL RESEARCH FOUNDATION, INC.) 26 June 1997, see entire document.	1-3, 5, 7, 9, 11, 13, 18-24, 27, 30, 33, 36, 39, 49-78
X	Database Caplus on STN, The American Chemical Society, No. 125:138016, LING, K. 'Coat protein gene indentification, genome organization, and pcr detection of grapevine leafroll associated cloterovirus-3 and study towards transgenic grapevines (vitis).	1-3
X	HABILI ET AL. Natural Spread and Molecular Analysis of Grapevine Leafroll-Associated Virus 3 in Australia. Phytopathology. November 1995, Volume 85, Number 11, pages 1418-1422, see entire document.	1-3, 20-23, 71-73, 75

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 17 SEPTEMBER 1998	Date of mailing of the international search report 14 OCT 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer ANISH GUPTA Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10313

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SALDARELLI ET AL. 'Detection of Grapevine Leafroll-Associated Closterovirus III by Molecular Hybridization' Plant Pathology, Volume 43, Number 1, pages 91-96, see entire document.	1-3
X	LING ET AL. 'Partial Genome Organization of Grapevine leafroll-associated clostervirus', Phytopathology, Volume 85, Number 10, page 1152, abstract number 302.	1-3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/10313

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 4, 6, 8, 10, 12, 14-17, 25-26, 28-29, 31-32, 34-35, 37-38, 40-48
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claimed subject matter is drawn to large amino acid or nucleotide sequences that require a sequence search. However the applicant has not complied with sequence listing requirement and therefore a sequence search could not be conducted.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10313

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 15/02, 15/11, 15/40, 15/54, 15/82; C07K 14/005, 14/01, 14/08, 16/08; C12Q 1/68; G01N 33/53

A. CLASSIFICATION OF SUBJECT MATTER: US CL :

514/2, 44; 530/350, 826; 536/22.1, 23.72; 424/130.1, 159.1; 435/ 172.2, 172.3, 410; 436/512

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

Group I , claim(s)1-3,5,7,9,11,13,18,AND 19, drawn to the polypeptide.

Group II, claim(s) 20-21, drawn to drawn to the RNA.

Group III, claim(s) 22-24, 27,30,33,36,and 39, drawn to DNA.

Group IV , claim(s)49-50, drawn to an expression system.

Group V, claim(s) 51-54, drawn to a host cell.

Group VI, claim(s)55-57, drawn to transgenic plant.

Group VII , claim(s)58-62, drawn to a method of imparting grapevine leafroll virus.

Group VIII, claim(s) 63-66, drawn to drawn to method of imparting beet yellows virus.

Group IX, claim(s) 67-70, drawn to method of imparting tristeza virus.

Group X, claim(s)71-72, drawn to an antibody.

Group XI, claim(s) 73-74, drawn to a method of detecting the grapevine leafroll virus utilizing an antibody.

Group XII, claim(s)75-78, drawn to a method of detecting the grapevine leafroll virus utilizing a nucleotide sequence.

The inventions listed as Groups I-XII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I, II, III, X are distinct in that they do not share a common structural core. Groups VII, VIII, IX are distinct in that each method utilizes a different viruses and thus the methods are different. Groups XI and XII are distinct in that the method of detection utilize different and structurally distinct compounds. Group XI utilizes a antibody while Group XII utilize a nucleotide sequence. Finally, Groups IV, V, and VI are distinct in that and they are structurally distinct from one another and they utilize different methods and techniques for achieving the desired product.